

From: O'Hara, Eileen  
Sent: Wednesday, September 18, 2002 5:39 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search request for 09/746,375

## SEARCH REQUEST FORM-SEQUENCE

Examiner: Eileen O'Hara (Room 10E18) Art Unit 1646

Serial Number: **09/746,375**  
**Novel Cytokine ZCYTO18**  
**Presnell et al**

Date: 09/18/02 Phone: 308-3312 CM1 10A01 mailbox 10C01

Please search the following:

SEQ ID NO: 1

also, 14 contiguous nucleotides of SEQ ID NO: 1

in commercial and interference databases.

Please put results on paper.

Thank you!

Eileen

*Eileen B. O'Hara*  
**CM1 10A01 mailbox 10C01**  
**703-308-3312**  
**U.S. Patent and Trademark Office**  
**Art Unit 1646**  
**eileen.o'hara@uspto.gov**

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

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SEP 19 2002  
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(STIC)

10019

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 9/19/02  
Date Completed: 10/3/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: 2  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 04  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 00:43:59 ; Search time 217.46 Seconds  
(without alignments)  
8811.168 Million cell updates/sec

Title: US-09-746-375-1

Perfect score: 1116

Sequence: 1 tcgagtttagaattgtctgca.....ataaacacttgatataocta 1116

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 14

Total number of hits satisfying chosen parameters: 19226

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	100.0	1116	22	Human cytokine, ZC
2	1116	100.0	1116	22	Human IL-TIF polyp
3	1116	100.0	1116	22	Human GIL-19/AE289
4	1114	99.8	1152	21	Human GIL-19/AE289
5	1114	99.8	1152	22	Human GIL-19/AE289
6	1090	97.7	1132	22	Nucleotide sequenc
7	934	83.7	1139	22	Human EXCS encodin
8	639	57.3	690	22	Human interleukin-
9	639	57.3	690	22	Human T cell induc
					Human cDNA encodin

10	207	18.5	4796	21	AAA28840	Human T cell induc
11	207	18.5	4797	22	AAS14876	Human partial geno
12	35	3.1	778	22	AAD09746	Mouse ZCYTO18 cDNA
13	35	3.1	1119	21	AAA28815	Murine T cell indu
14	35	3.1	1119	22	AAS14858	Mouse cDNA encodin
15	35	3.1	1166	21	AAC81774	Murine GIL-19 prot
16	31	2.8	7444	21	AAA28816	Murine T cell indu
17	31	2.8	7445	22	AAS14859	Mouse partial geno
18	28	2.5	1111	21	AAA28817	Murine T cell indu
19	28	2.5	1111	22	AAS14860	Mouse cDNA for T c
20	28	2.5	5935	21	AAA28818	Murine T cell indu
21	28	2.5	5935	22	AAS14878	Mouse partial geno
22	27	2.4	36	22	AAD09730	Human ZCYTO18 cDNA
23	27	2.4	36	22	AAF83753	Human IL-TIF cDNA
24	24	2.2	24	22	AAD09721	PCR primer, ZC2584
25	24	2.2	24	22	AAD09722	PCR primer, ZC2584
26	24	2.2	33	22	AAD09731	Human ZCYTO18 cDNA
27	24	2.2	33	22	AAF83754	Human IL-TIF cDNA
28	24	2.2	5421	24	ABL32132	Human immune syste
29	23	2.1	23	22	AAD09724	ZC25839 PCR primer
30	23	2.1	37	22	AAD09734	Human ZCYTO18 cDNA
31	22	2.0	22	21	AAA28831	Primer for human T
32	22	2.0	22	22	AAS14867	Human T cell deriv
33	22	2.0	39	22	AAD09733	Human ZCYTO18 cDNA
34	22	2.0	2640	22	AAH76178	A. thaliana SGT101
35	22	2.0	2671	22	AAH76176	A. thaliana SGT101
36	21	1.9	21	21	AAA28833	5' RACE primer for
37	21	1.9	21	21	AAA28834	5' RACE primer for
38	21	1.9	21	21	AAS14869	Human T cell deriv
39	21	1.9	21	22	AAS14870	Human T cell deriv
40	21	1.9	706	22	AAH57394	Human skeletal mus
41	21	1.9	3126	21	AAA70143	Plasmodium falcipa
42	21	1.9	15768	24	ABL33171	Human immune syste
43	21	1.9	16217	24	ABL32625	Human immune syste
44	20	1.8	473	22	ABA43453	Human breast cell
45	20	1.8	473	22	ABA53906	Human foetal liver

#### ALIGNMENTS

RESULT 1  
AAD09719  
ID AAD09719 standard; cDNA; 1116 BP.  
XX  
AC AAD09719;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human cytokine, ZCYTO18 cDNA.  
XX  
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;  
cancer; inflammation; gene therapy; chromosome 12; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 21..560  
FT /\*tag= a  
FT /product= "Human ZCYTO18 protein #1"  
FT 21..119  
FT /\*tag= b  
FT 120..557  
FT /\*tag= c  
FT /product= "Human mature ZCYTO18 protein #1"  
FT 57..560  
FT /\*tag= d  
FT /product= "Human ZCYTO18 protein #2"  
FT 57..119  
FT /\*tag= e  
FT 120..557  
FT /\*tag= f  
FT /product= "Human mature ZCYTO18 protein #2"



```
XX (ZYMO ) ZYMOGENETICS INC.
PA Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
XX WPI; 2001-356158/37.
DR P-PSDB; AAB62664.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions -
XX
XX Example 17; Page 193-195; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC inflammatory response in a mammal with inflammation. Heteromeric/
CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC can also be used to detect IL-TIF levels which is indicative of
CC pathological conditions including inflammatory states (e.g. rheumatoid
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC polypeptides themselves are useful for the treatment of inflammation,
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC diseases. The antibodies and zcytor16 polynucleotides are also useful
CC for detecting cancer. The present sequence represents a cDNA encoding
CC the human IL-TIF protein.
XX
SQ Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;
```

```
Query Match 100.0%; Score 1116; DB 22; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 541 tgagaaatgcctgctgatttgaccagagcaaaagctgaaatgaataactaacccctttcc 600
QY 601 ctgctagaaataacaattagatgccccaaagcgatttttttaacccaaaggaagatggg 660
Db 601 ctgctagaaataacaattagatgccccaaagcgatttttttaacccaaaggaagatggg 660
QY 661 aagccaaactccatcatgatgggtgattccaaaatgaaccctcggttagtlacaaagga 720
Db 661 aagccaaactccatcatgatgggtgattccaaaatgaaccctcggttagtlacaaagga 720
QY 721 aaccatgacacttttcttataagaccagaaggtagactttcttaagcagatagatttat 780
Db 721 aaccatgacacttttcttataagaccagaaggtagactttcttaagcagatagatttat 780
QY 781 tgataacatttctgaactggtgtctctatcacagaaaaacaatttatttttaataaa 840
Db 781 tgataacatttctgaactggtgtctctatcacagaaaaacaatttatttttaataaa 840
QY 841 ttgtctttttccataaaaaagattcttccattctttaggggaaaaaacccctaaata 900
Db 841 ttgtctttttccataaaaaagattcttccattctttaggggaaaaaacccctaaata 900
QY 901 gcttcattgtttccataaactcagctacttattattataaattgtattattattataaga 960
Db 901 gcttcattgtttccataaactcagctacttattattataaattgtattattattataaga 960
QY 961 ctgcattttatttatcatcttttatttaataatgatgattttattatagaacatcattgata 1020
Db 961 ctgcattttatttatcatcttttatttaataatgatgattttattatagaacatcattgata 1020
QY 1021 ttgctacttgagttaaggctaataattgataatttataacataattatagagctataaca 1080
Db 1021 ttgctacttgagttaaggctaataattgataatttataacataattatagagctataaca 1080
QY 1081 tgtttatttgacctcaataaacaacttggatcccta 1116
Db 1081 tgtttatttgacctcaataaacaacttggatcccta 1116
RESULT 3
AAC81773
ID AAC81773 standard; cDNA; 1177 BP.
XX AC AAC81773;
XX DT 23-FEB-2001 (first entry)
XX Human GIL-19/AE289 protein coding sequence.
DE DE
XX KW Human; GIL-19/AE289; IL-10; interleukin-10; nutrition;
KW cell proliferation; immune stimulation; immune suppression;
KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.
XX OS Homo sapiens.
XX PN WO200065027-A2.
XX PD 02-NOV-2000.
XX PF 28-APR-2000; 2000WO-US11479.
XX PR 28-APR-1999; 99US-0131473.
XX PA (GENY ) GENETICS INST INC.
XX PI Jacobs K, Fouser L, Spaulding V, Xuan D;
XX WPI; 2000-687325/67.
DR P-PSDB; AAB36292.
```

XX Human GIL-19 protein that shows a high degree of homology to IL  
PT (interleukin)-10, useful in upregulation of humoral immune responses,  
PT as an antiinflammatory agent and as a modulator of immune responses  
PT associated with injury -  
XX  
PS  
PS  
XX Claim 1; Page 59; 60pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC novel human GIL-19/AE289 protein. The protein shows homology to  
CC interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used  
CC in the regulation of cell proliferation and differentiation,  
CC haematopoiesis, immune stimulation or suppression, tissue growth and  
CC tumour inhibition. In addition, it also has uses in the treatment of  
CC inflammation and in nutrition.  
XX  
XX Sequence 1177 BP; 362 A; 245 C; 232 G; 338 T; 0 other;  
SQ

Query Match 100.0%; Score 1116; DB 21; Length 1177;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcgagttgagattgtctgcaatggccgcccctgcagaaatctgtgagcttttccattgg 60  
DB 45 tcgagttgagattgtctgcaatggccgcccctgcagaaatctgtgagcttttccattgg 104  
QY 61 ggaacctggccaccagctgctctctcttcttggccctcttggtacagggagagcagctg 120  
DB 105 ggaacctggccaccagctgctctctcttcttggccctcttggtacagggagagcagctg 164  
QY 121 cgcccatcagctcccatcgaggcttgacagtcacacttccagccctatatacaca 180  
DB 165 cgcccatcagctcccatcgaggcttgacagtcacacttccagccctatatacaca 224  
QY 181 accgcaccttcattgctggtaagagagctagcttggtgatacaacacagacgttgcgc 240  
DB 225 accgcaccttcattgctggtaagagagctagcttggtgatacaacacagacgttgcgc 284  
QY 241 tcattggggagagaactgttcacagagtcagtatgagtgagcgtctgctatctgatgaagc 300  
DB 285 tcattggggagagaactgttcacagagtcagtatgagtgagcgtctgctatctgatgaagc 344  
QY 301 aggtgctgaacttcaccccttgagaagtgctgttccctcaatctgtaggttccagcctc 360  
DB 345 aggtgctgaacttcaccccttgagaagtgctgttccctcaatctgtaggttccagcctc 404  
QY 361 atatgcagagaggtgtgcttcccttctggccagctcagcaacagcgttaagcacatgtcata 420  
DB 405 atatgcagagaggtgtgcttcccttctggccagctcagcaacagcgttaagcacatgtcata 464  
QY 421 ttgaagggtgatgacctgcataatccagaggaatgtgcaaaaagctgaaggacacagtgaaaa 480  
DB 465 ttgaagggtgatgacctgcataatccagaggaatgtgcaaaaagctgaaggacacagtgaaaa 524  
QY 481 agcttggagagagtgagagatcaaaagcaatggagaaactggagattgtgtttatgtctc 540  
DB 525 agcttggagagagtgagagatcaaaagcaatggagaaactggagattgtgtttatgtctc 584  
QY 541 tgagaaatgcttgcatttgaccagagcaagctgaaatgaataactaacccctttcc 600  
DB 585 tgagaaatgcttgcatttgaccagagcaagctgaaatgaataactaacccctttcc 644  
QY 601 ctgctagaaaaaacaattagatgcccaagcgatttttttaacccaaaggaagatggg 660  
DB 645 ctgctagaaaaaacaattagatgcccaagcgatttttttaacccaaaggaagatggg 704  
QY 661 aagccaaactccatcatgatgggtggattccaaaatgaaccctcggttagttacaagga 720  
DB 705 aagccaaactccatcatgatgggtggattccaaaatgaaccctcggttagttacaagga 764  
QY 721 aaccatgcacatttttttaaacacagagaggttagacctttcttaagcatagatatattat 780

DB 765 aaccaatgccacttttgtttataaagaccaggaaggtagaactttctaaagcatagatttat 824  
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DB 825 tgatacaattctattgtaactgtgttctctatcacagagaaacaatttttttaataaa 884  
QY 841 ttgtctttttccataaaaaagattacttctccattcccttaggggaaaaaacccctaaata 900  
DB 885 ttgtctttttccataaaaaagattacttctccattcccttaggggaaaaaacccctaaata 944  
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DB 945 gctcatgtttccataaatcagtcactttattattataaaatgtattattattataaga 1004  
QY 961 ctgcattttatttatcatcattttattataatgatgattattattatagaacaatcattcgata 1020  
DB 1005 ctgcattttatttatcatcattttattataatgatgattattattatagaacaatcattcgata 1064  
QY 1021 ttgctacttgagtgtaagcgttagtattgataatttattgacaataattatagagctataaca 1080  
DB 1065 ttgctacttgagtgtaagcgttagtattgataatttattgacaataattatagagctataaca 1124  
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AAF921134  
ID AAF921134 standard; cDNA; 1152 BP.  
XX  
AC AAF921134;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Human PRO10096 cDNA.  
XX  
KW Human; PRO protein; mapping; ss.  
XX  
OS Homo sapiens.  
PN WO200116318-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 24-AUG-2000; 2000WO-US23328.  
XX  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 07-DEC-1999; 99US-0169495.  
PR 09-DEC-1999; 99US-0170262.  
PR 11-JAN-2000; 2000US-0175481.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 03-MAR-2000; 2000US-0187202.  
PR 25-APR-2000; 2000US-0199397.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 05-JUN-2000; 2000US-0209832.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
XX  
XX WPI; 2001-183260/18.  
DR P-PSDB; AAB87602.  
XX  
XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
PT chromosome and gene mapping.  
XX

PS Claim 2; Fig 153; 278pp; English.

XX The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

XX Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;

Query Match 99.8%; Score 1114; DB 22; Length 1152;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcgagttagaattgtctgcaatggcgccctgcagaaatctgtgagctttcccttatgg 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
38 tcgagttagaattgtctgcaatggcgccctgcagaaatctgtgagctttcccttatgg 97  
QY 61 ggacctggccaccagctgcctccctctcttggccctctgtgtacaggagagcagctg 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
98 ggacctggccaccagctgcctccctctcttggccctctgtgtacaggagagcagctg 157  
QY 121 cggccatcagctcccaactgcagcttgacaagctccaaactccagcagccctatacaca 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
158 cggccatcagctcccaactgcagcttgacaagctccaaactccagcagccctatacaca 217  
QY 181 accgcaactctatgtctgctgaaggagctgtgctgtgatacaacacagacgttcgtc 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
218 accgcaactctatgtctgctgaaggagctgtgctgtgatacaacacagacgttcgtc 277  
QY 241 tcattggggagaaactgtccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
278 tcattggggagaaactgtccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 337  
QY 301 aggtgtcgaactccactcccttgaagagtgctgttccctcaactctgataaggttccagcctt 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
338 aggtgtcgaactccactcccttgaagagtgctgttccctcaactctgataaggttccagcctt 397  
QY 361 atatcagagagtggtgctccctccctgcccagctcagcaacaggttaagcagcatgtcata 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
398 atatcagagagtggtgctccctccctgcccagctcagcaacaggttaagcagcatgtcata 457  
QY 421 ttgaaggtgatgacctgcataatccagaggaatgtgcataaagctgaaggacagtgaaaa 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
458 ttgaaggtgatgacctgcataatccagaggaatgtgcataaagctgaaggacagtgaaaa 517  
QY 481 agcttggagagagtgagagatcaagcaaatgggagaaactggtattgtctgtttatgtctc 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
518 agcttggagagagtgagagatcaagcaaatgggagaaactggtattgtctgtttatgtctc 577  
QY 541 tgagaaatgctctgatttgaccagagcaagctgaaatgaataactaacccccctttcc 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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QY 601 ctgctagaaataaactatagatgcccacaaagcgatatttttaacaaagaagatggg 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
638 ctgctagaaataaactatagatgcccacaaagcgatatttttaacaaagaagatggg 697  
QY 661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
698 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 757  
QY 721 aaccaatgccaactttgtttataagaccagaaggtagactttcttaagcatagatatattat 780  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
758 aaccaatgccaactttgtttataagaccagaaggtagactttcttaagcatagatatattat 817  
QY 781 tgataaacatttcatctgaactggttcttatatacagaaaaaacaaatttttttaataaa 840  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 818 tgataaacatttcatgttaactggtgttctatacagaaaaacaattattttttaataa 877  
QY 841 ttgtctttttccataaaaaagattactttcccttcttcttcttcttcttcttcttcttctt 900  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
878 ttgtctttttccataaaaaagattactttcccttcttcttcttcttcttcttcttcttctt 937  
QY 901 gttctatgtttccataaaatcagtcactttattattattataaaatgtattattattataaga 960  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
938 gttctatgtttccataaaatcagtcactttattattattataaaatgtattattattataaga 997  
QY 961 ctgcattttttattattattattattattattattattattattattattattattattatt 1020  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
998 ctgcattttttattattattattattattattattattattattattattattattattatt 1057  
QY 1021 ttgtctacttgagtgtaaggcctaattattattattattattattattattattattattatt 1080  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1058 ttgtctacttgagtgtaaggcctaattattattattattattattattattattattattatt 1117  
QY 1081 tgtttatttgacctcaataaacaacttggatatcc 1114  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1118 tgtttatttgacctcaataaacaacttggatatcc 1151  
RESULT 5  
AAC87053  
ID AAC87053 standard; cDNA; 1152 BP.  
XX  
AC AAC87053;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of human polypeptide PRO10096.  
XX  
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;  
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;  
KW PRO1188; PRO1272; PRO1419; PRO4999; PRO170; PRO248; PRO353; PRO1318;  
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;  
KW PRO246; PRO265; PRO341; PRO10096; PRO6003; PRO6004; PRO350; PRO3630;  
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 58..597  
FT sig\_peptide 58..156 /\*tag= a  
FT /\*tag= b  
XX  
PN WO200077037-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 22-MAY-2000; 2000WO-US14042.  
XX  
PR 15-JUN-1999; 99US-0139695.  
PR 20-JUL-1999; 99US-0145070.  
PR 26-JUL-1999; 99US-0145698.  
PR 17-AUG-1999; 99US-0149396.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28565.  
PR 07-DEC-1999; 99US-0169495.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR

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PR 20-MAR-2000: 2000WO-US07377.
PR 30-MAR-2000: 2000WO-US08439.
PR 15-MAY-2000: 2000WO-US13358.
PR 17-MAY-2000: 2000WO-US13705.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnovers L, Eaton DL;
XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Kijavlin IJ, Mather JP, Napier MA, Pan J;
XX Paooni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
XX Wood WI, Zhang Z;
XX
XX WPI: 2001-050091/06.
XX P-PSDB: AAB31210.
XX
XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a
XX transmembrane polypeptide is useful for gene therapy and identification
XX of related polypeptides .
XX
XX Claim 2; Fig 63; 244pp; English.
XX
XX The present sequence encodes a human secreted and transmembrane
XX polypeptide. The specification describes human polypeptides, designated
XX PRO196, PRO444, PRO183, PRO185, PRO210, PRO217, PRO242, PRO286,
XX PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
XX PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
XX PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
XX PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
XX can be modulated with agents that bind to these polypeptides, resulting
XX in the death of the cells. The polynucleotides encoding of these
XX polypeptides are useful in the recombinant production of the
XX polypeptides, as a hybridisation probe to screen libraries to isolate
XX homologous sequences, or to map the gene. They may also be used for
XX analysing genetic disorders, and to produce transgenic animals which are
XX useful for the development and screening of therapeutically useful
XX reagents. The polynucleotides can also be used in gene therapy e.g. to
XX replace a defective gene.
XX
XX Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other:
XX
XX Query Match 99.8%; Score 1114; DB 22; Length 1152;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 tcgagttagaattctgtcaatggccgctcgacgaatactgtgagctcttccctatgg 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 38 tcgagttagaattctgtcaatggccgctcgacgaatactgtgagctcttccctatgg 97
XX
XX 61 ggacctggccaccagctgctctctctcttggccctcttggtagcaggaggagcagctg 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 98 ggacctggccaccagctgctctctctcttggccctcttggtagcaggaggagcagctg 157
XX
XX 121 ggcctatcagctcccaactgcaggcttgcaagtcgaagtcgaagtcgaagtcgaagtc 180
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 158 ggcctatcagctcccaactgcaggcttgcaagtcgaagtcgaagtcgaagtcgaagtc 217
XX
XX 181 accgacattctatgctgagcaggagctgctgctgctgctgctgctgctgctgctgct 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 218 accgacattctatgctgagcaggagctgctgctgctgctgctgctgctgctgctgct 277
XX
XX 241 tcattggggagaaactgttccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 278 tcattggggagaaactgttccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 337
XX
XX 301 aggtgctgaactcacccttgaagaagtgctgttccctcctcaatctgataggttccagcctt 360
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 338 aggtgctgaactcacccttgaagaagtgctgttccctcctcaatctgataggttccagcctt 397
XX
XX 361 atatcaggaggtgtgtcccttccctggccagctcagcaaacagcagtcagtcagtcagtc 420
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 398 atatcaggaggtgtgtcccttccctggccagctcagcaaacagcagtcagtcagtcagtc 457

```

## RESULT 6

AAC84310

ID AAC84310 standard; cDNA; 1132 BP.

XX

XX AAC84310;

XX

XX 19-MAR-2001 (first entry)

XX

XX Human EXCS encoding cDNA (clone ID 5571181CB1).

XX

XX Extracellular signaling molecule; EXCS; anti-inflammatory; human;  
 XX immunosuppressive; cytostatic; neuroprotective; gastrointestinal;  
 XX viricide; antibacterial; anti-HIV; human immunodeficiency virus;  
 XX antileukemia; cerebroprotective; neurotropic; antitumor; antifungal;  
 XX anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;  
 XX keratolytic; protozoicide; gene therapy; ss.

XX Homo sapiens.

XX OS

XX

XX WO200070049-A2.

XX

XX 23-NOV-2000.

XX



PF 19-MAY-2000; 2000WO-US13975.  
 XX 19-MAY-1999; 99US-0134949.  
 PR 15-JUL-1999; 99US-0144270.  
 PR 30-JUL-1999; 99US-0146700.  
 XX 04-OCT-1999; 99US-0157508.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;  
 PI Azimzai Y, Lu DAM, Patterson C;  
 PI WPI: 2001-025021/03.  
 XX P-PSDB; AAB48074.  
 PT New human extracellular signaling nucleic acids and polypeptides useful  
 PT for diagnosing, treating and preventing infections and  
 PT gastrointestinal, neurological, reproductive, and  
 PT autoimmune/inflammatory disorders  
 XX Claim 4; Page 108; 114pp; English.  
 PS The invention provides human extracellular signaling molecules (EXCS)  
 CC and polynucleotides which identify and encode EXCS. EXCS can be  
 CC expressed by standard recombinant methodology. The amino acid and nucleic  
 CC acid sequences of EXCS are useful for diagnosing, treating and  
 CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,  
 CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular  
 CC disease, stroke), reproductive (infertility, ovulatory defects,  
 CC emmenoriosis), autoimmune/inflammatory (actinic keratosis, acquired  
 CC immunodeficiency syndrome (AIDS), Addison's disease), and cell  
 CC proliferative disorders including cancers (of the breast, adrenal gland,  
 CC bone). They may also be used to treat fatal familial insomnia,  
 CC nutritional and metabolic diseases of the nervous system, myopathies,  
 CC mental disorders (anxiety, schizophrenia, mood), as well as infections  
 CC caused by parasites (malaria, leishmania, trypanosoma), viral  
 CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,  
 CC staphylococcus, bacillus), and fungal (aspergillus, blastomycetes, etc.)  
 CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,  
 CC agonists, pharmaceutical compositions, and antibodies may also be used  
 CC for treating or preventing disorders associated with increased or  
 CC decreased expression or activity of EXCS. EXCS polynucleotides may also  
 CC be used to detect and quantify gene expression in biopsied tissues in  
 CC which expression of EXCS may be correlated with the disease, to determine  
 CC presence or excess expression of EXCS, to monitor regulation of EXCS  
 CC levels during therapeutic intervention, to detect the presence of  
 CC associated disorders, as targets in microarray, to generate hybridization  
 CC probes, and to detect differences in gene sequences among normal, carrier  
 CC or affected individuals. Antibodies may also be used in diagnosing  
 CC disorders, in monitoring patients being treated with EXCS agonists,  
 CC antagonists or inhibitors. Sequences AAC84293-C84318 represent nucleic  
 CC acid molecules encoding the EXCS of the invention.  
 XX  
 XX Sequence 1132 BP; 333 A; 240 C; 236 G; 333 T; 0 other;

Query Match 97.7%; Score 1090; DB 22; Length 1132;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 tcgagttagaattgtctgaatggccgcctgcagaaatctgtgagctcttccattgg 60  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 31 tcgagttagaattgtctgaatggccgcctgcagaaatctgtgagctcttccattgg 90  
 QY 61 ggacctggccaccagctccctctctcttggccctctgtgacaggagagcagctg 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 91 ggacctggccaccagctccctctctcttggccctctgtgacaggagagcagctg 150  
 QY 121 cgccatcagctcccaactgagcttgcagaaactccagcagccctataacca 180  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 151 cgccatcagctcccaactgagcttgcagaaactccagcagccctataacca 210  
 QY 181 accgcacctctatgctggttaaggaggttagcttggctgatacaacacagcgttcg 240  
 XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 XX

Db 211 accgcacctctatgctggttaaggaggttagcttggctgatacaacacagcgttcg 270  
 QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 241 tcattggggagaaactgttccacggagtcagtatgagtgagcgtctctatcgtgaagc 300  
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 271 tcattggggagaaactgttccacggagtcagtatgagtgagcgtctctatcgtgaagc 330  
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 331 agtgctgaacttcaccttgaagaagtgctgttccctcaatctgatatggttccagcctt 390  
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 361 atatgcagagagtggtgcttcccttccctgcaggtcagcaacacaggttaagcacatgcatca 420  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 391 atatgcagagagtggtgcttcccttccctgcaggtcagcaacacaggttaagcacatgcatca 450  
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 421 ttgaagtgatgacctgcatactccagaggaatgtgcaaaagctgaaaggtgacacagtgaaaaa 480  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 451 ttgaagtgatgacctgcatactccagaggaatgtgcaaaagctgaaaggtgacacagtgaaaaa 510  
 QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 481 agcttgagagagtggtgagagatcaaaagcaatgtggagaactggtattgtgttattgtctc 540  
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 511 agcttgagagagtggtgagagatcaaaagcaatgtggagaactggtattgtgttattgtctc 570  
 QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 541 tgagaaatcctgcatttgaccagagcaaaagctgaaaaatgataactaaccccttctcc 600  
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 961 ctgcattttattatcatcttttattataatgattttattataaaatcatttcgata 1020  
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 991 ctgcattttattatcatcttttattataatgattttattataaaatcatttcgata 1050  
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 1051 ttgtctacttgagtgtaaggctaatattgattattatgacaataattatagagctataaca 1110  
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 1081 tgtttatttg 1090  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1111 tgtttatttg 1120

RESULT 7  
 AAF28841  
 ID AAF28841 standard; DNA; 1139 BP.  
 XX  
 AC AAF28841;  
 XX  
 DT 25-APR-2001 (first entry)  
 XX  
 DE Human interleukin-10 homologue IL-D110 DNA sequence.



AAA28839 standard; cDNA; 690 BP.  
 AAA28839;  
 04-SEP-2000 (first entry)  
 Human T cell inducible factor cDNA.  
 TIF-alpha; T cell derived inducible factor; Interleukin 9; STAT; IL-9;  
 Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;  
 probe; chromosome 12q15; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 72..611  
 /\*tag= a

WO200024758-A1.  
 04-MAY-2000.  
 18-OCT-1999; 99WO-US24424.  
 26-OCT-1998; 98US-0178973.  
 16-JUL-1999; 99US-0354243.  
 (LUDW-) LUDWIG INST CANCER RES.  
 Dumoutier L, Louhed J, Renaud J;  
 WPI; 2000-422495/36.  
 P-PSDB; AAY92879.

New nucleic acid molecule encoding a T cell derived inducible factor  
 for treating asthma, an allergy or lymphoma  
 Claim 1; Page 38; 46pp; English.

This cDNA encodes a human T cell derived inducible factor (TIF). The gene  
 was mapped to chromosome 12q15. The human TIF was identified based on  
 homology to a murine TIF, which was identified by subtraction cloning  
 from a murine lymphoma cell line BW5147 in the presence or absence of  
 interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to  
 add any cytokines to its culture medium. Many IL-9 activities are  
 mediated by activation of STAT transcription factors. The novel TIFs were  
 expressed in the presence of IL-9, but not in its absence. TIFs induce  
 STAT activation in cells. They can be used, e.g. in the stimulation of  
 regeneration of targeted tissues. Their inhibitors or antagonists can be  
 used to retard, prevent or inhibit differentiation of other tissues. The  
 TIFs and their coding sequences are useful in the treatment of asthma,  
 allergies and lymphoma (claimed). They are also useful for identifying  
 compounds that inhibit or activate T cell induced factor activity in a  
 cell (claimed).

Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

Query Match 57.3%; Score 639; DB 21; Length 690;  
 Best Local Similarity 100.0%; Pred. No. 2e-301;  
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 tcgagttagaattgctgcaatgccgcctcgcaaatctgtgagctcttctctatgg 60  
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 61 ggaacctggccaccagctgcctctctcttcttggccctcttgggtacaggagcagctg 120  
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 112 ggaacctggccaccagctgcctctctcttcttggccctcttgggtacaggagcagctg 171  
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 121 cgcccatcagctccctcagctgagcttgcacagttcccaactccagaccctatcacca 180  
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 172 cgcccatcagctccctcagctgagcttgcacagttcccaactccagaccctatcacca 231  
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181 accgcaccttcatgctgaagagagctggtggtgatacaacaacacagcttcgtc 240  
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 241 tcattggggagaactgttccacggagtcagtcagtcagtcagtcagtcagtcagtc 300  
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 292 tcattggggagaactgttccacggagtcagtcagtcagtcagtcagtcagtcagtc 351  
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 361 atatgcaggagtggtgcttctcctgcccaggtcagcaacaggtcagtcagtcagtc 420  
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 412 atatgcaggagtggtgcttctcctgcccaggtcagcaacaggtcagtcagtcagtc 471  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 421 ttgaagtgatgacctgcatactcagaggaatgtgcaaaagctgaagacacagtcgaa 480  
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 472 ttgaagtgatgacctgcatactcagaggaatgtgcaaaagctgaagacacagtcgaa 531  
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 481 agcttgagagagtgagagatcaaacgaattggagaaactgattgctgttattgtctc 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 532 agcttgagagagtgagagatcaaacgaattggagaaactgattgctgttattgtctc 591  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 541 tgagaaatgctgctgatttgaccagagcaaaagctgaaaaatgaataaactaaccccttcc 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 592 tgagaaatgctgctgatttgaccagagcaaaagctgaaaaatgaataaactaaccccttcc 651  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 601 ctgctagaataacaattagatgccccaaagcgattttt 639  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 652 ctgctagaataacaattagatgccccaaagcgattttt 690  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9  
 AAS14875  
 ID AAS14875 standard; cDNA; 690 BP.  
 XX  
 AC AAS14875;  
 XX  
 DT 19-DEC-2001 (first entry)  
 XX  
 DE Human cDNA encoding T cell derived inducible factor, TIF.  
 XX  
 KW Human; T cell derived inducible factor; TIF; ss; antiasthmatic;  
 KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;  
 KW cancer; lymphoma; immune system disorder; allergy; asthma; diabetes;  
 KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;  
 KW thyroiditis; melanoma; hepatoma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 72..611  
 FT /\*tag= a  
 FT /product= "TIF"  
 FT /transl\_except= (pos:159..161,aa:Glu)  
 FT /transl\_except= (pos:378..380,aa:Ile)  
 FT /transl\_except= (pos:405..407,aa:Arg)  
 FT /transl\_except= (pos:519..521,aa:Cys)  
 XX  
 PN US2001024652-A1.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 29-DEC-2000; 2000US-0751797.  
 XX  
 PR 18-OCT-1999; 99US-0419568.  
 PR 26-OCT-1998; 98US-0178973.  
 PR 16-JUL-1999; 99US-0354243.  
 XX  
 PA (DUMO/) DUMOUTIER L.  
 PA (LOUA/) LOUAHED J.

(RENA/) RENAULD J.  
Dumontier L, Louhed J, Renauld J;  
WPI: 2001-638496/73.  
P-PSDB; AAU09091.  
New isolated nucleic acid molecules encoding T cell inducible factors,  
useful as markers for expression or effect of interleukin (IL)-9, in a  
subject and diagnosing susceptibility to asthma or allergy  
Claim 1: Page 17; 26pp; English.  
The invention relates to an isolated nucleic acid molecule, which encodes  
a T cell derived inducible factor (TIF) which are upregulated by the  
cytokine interleukin-9 (IL-9) and induce STAT transcription factor  
activation. The TIF proteins (or their mutants) may be used to test IL-9  
antagonists for their potency against lymphomas, immune system  
disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),  
autoimmune diabetes and thyroiditis. TIF molecules promote regeneration  
or inhibit differentiation of tissue types in which they are active and  
therefore be used to develop treatments for melanomas and hepatomas.  
The present sequence encodes human TIF.  
Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;  
Query Match 57.3%; Score 639; DB 22; Length 690;  
Best Local Similarity 100.0%; Pred. NO. 2e-301;  
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 tcgagttagaaatgtctgcaatggcgccctgcagaaatctgtgagctcttcttctatgg 60  
Db 52 tcgagttagaaatgtctgcaatggcgccctgcagaaatctgtgagctcttcttctatgg 111  
Qy 61 ggacccctggccacagctgctctctctcttcttgcctcttgggtacagggaggagcagctg 120  
Db 112 ggacccctggccacagctgctctctcttcttgcctcttgggtacagggaggagcagctg 171  
Qy 121 cggccatcagctccactgcagcttgacagcttcacaaactccacagcctctatcacca 180  
Db 172 cggccatcagctccactgcagcttgacagcttcacaaactccacagcctctatcacca 231  
Qy 181 accgacacttcagctggctgaagagctagcttgctgatacaacacagacgttcgct 240  
Db 232 accgacacttcagctggctgaagagctagcttgctgatacaacacagacgttcgct 291  
Qy 241 tcattggggagaaactgttccacagagctagctagctgagcgtctgtatctgatgaagc 300  
Db 292 tcattggggagaaactgttccacagagctagctagctgagcgtctgtatctgatgaagc 351  
Qy 301 aggtgctgaactccactgcagcttgacagctgcttccctcaatctgaggttccagcctt 360  
Db 352 aggtgctgaactccactgcagcttgacagctgcttccctcaatctgaggttccagcctt 411  
Qy 361 atatgcaggagggtggtgcttccctgcagagctcagcaacagagctgaagcactgtcata 420  
Db 412 atatgcaggagggtggtgcttccctgcagagctcagcaacagagctgaagcactgtcata 471  
Qy 421 ttgaaggtgatgactgcatactcagaggaatgtgcgcaaaagctgaagagacagtgaaaa 480  
Db 472 ttgaaggtgatgactgcatactcagaggaatgtgcgcaaaagctgaagagacagtgaaaa 531  
Qy 481 agcttgagagagtgagagatcaaaagcaattggagactgattgtgttattgtctc 540  
Db 532 agcttgagagagtgagagatcaaaagcaattggagactgattgtgttattgtctc 591  
Qy 541 tgaagaatgctgctatttgaccagagcaaaagctgaaaaatgaataactaaaccccttcc 600  
Db 592 tgaagaatgctgctatttgaccagagcaaaagctgaaaaatgaataactaaaccccttcc 651  
Qy 601 ctgctagaaaaatacaattagatgcccaaaagcagattttt 639  
Db 639 ctgctagaaaaatacaattagatgcccaaaagcagattttt 690  
Db 652 ctgctagaaaaatacaattagatgcccaaaagcagattttt 690  
RESULT 10  
AAA28840  
ID AAA28840 standard; DNA: 4796 BP.  
XX  
AC AAA28840;  
DT 04-SEP-2000 (first entry)  
XX  
DE Human T cell inducible factor genomic DNA.  
XX  
TIF; T cell derived inducible factor; Interleukin 9; STAT; IL-9;  
KW Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;  
KW probe; chromosome 12q15; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 108..4717  
FT /\*tag= a  
FT 1..257  
FT /\*tag= b  
FT 258..688  
FT /\*tag= c  
FT 689..754  
FT /\*tag= d  
FT 755..870  
FT /\*tag= e  
FT 871..1014  
FT /\*tag= f  
FT 1015..1938  
FT /\*tag= g  
FT 1939..2004  
FT /\*tag= h  
FT 2005..3837  
FT /\*tag= i  
FT 3838..4796  
FT /\*tag= j  
XX  
WO200024758-A1.  
XX  
PD 04-MAY-2000.  
XX  
PF 18-OCT-1999; 99WO-US24424.  
XX  
PR 26-OCT-1998; 98US-0178973.  
PR 16-JUL-1999; 99US-0354243.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Dumoutier L, Louhed J, Renauld J;  
XX  
WPI: 2000-422495/36.  
DR P-PSDB; AAY92879.  
XX  
PT New nucleic acid molecule encoding a T cell derived inducible factor  
PT for treating asthma, an allergy or lymphoma  
XX  
PS Claim 1; Page 39-40; 46pp; English.  
XX  
CC This DNA encodes a human T cell derived inducible factor (TIF). The gene  
CC was mapped to chromosome 12q15. The human TIF was identified based on  
CC homology to a murine TIF, which was identified by subtraction cloning  
CC from a murine lymphoma cell line BW5147 in the presence or absence of  
CC interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to  
CC add any cytokines to its culture medium. Many IL-9 activities are  
CC mediated by activation of STAT transcription factors. The novel TIFs were  
CC expressed in the presence of IL-9, but not in its absence. TIFs induce  
CC STAT activation in cells. They can be used, e.g. in the stimulation of  
CC regeneration of targeted tissues. Their inhibitors or antagonists can be  
CC used to retard, prevent or inhibit differentiation of other tissues. The

CC TIFs and their coding sequences are useful in the treatment of asthma,  
CC allergies and lymphoma (claimed). They are also useful for identifying  
CC compounds that inhibit or activate T cell induced factor activity in a  
CC cell (claimed).

XX Sequence 4796 BP; 1339 A; 912 C; 1063 G; 1482 T; 0 other;

Query Match 18.5%; Score 207; DB 21; Length 4796;  
Best Local Similarity 100.0%; Pred. No. 9.6e-91;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcgagttagaattgtctgcaatggcgccctgcagaaatctgtgagctcttccctatgg 60

Db 52 tcgagttagaattgtctgcaatggcgccctgcagaaatctgtgagctcttccctatgg 111

Qy 61 ggacctggccaccagctgctccctctcttggccctctgtgtacaggagagcagctg 120

Db 112 ggacctggccaccagctgctccctctcttggccctctgtgtacaggagagcagctg 171

Qy 121 cggccatcagctcccaactgcaggttgacaagtccaactccagcagccctatacaca 180

Db 172 cggccatcagctcccaactgcaggttgacaagtccaactccagcagccctatacaca 231

Qy 181 accgcaccttcagctggctaaggagg 207

Db 232 accgcaccttcagctggctaaggagg 258

## RESULT 11

AAAS14876  
ID AAAS14876 standard; DNA; 4797 BP.

XX AC AAAS14876;

XX DT 19-DEC-2001 (first entry)

XX DE Human partial genomic DNA for T cell derived inducible factor, TIF.

XX KW Human; T cell derived inducible factor; TIF; ds; antiallergic;  
KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;  
KW cancer; lymphoma; immune system disorder; allergy; asthma;  
KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;  
KW thyroiditis; melanoma; hepatoma.

XX OS Homo sapiens.

XX PN US2001024652-A1.

XX PD 27-SEP-2001.

XX PF 29-DEC-2000; 2000US-0751797.

XX PR 18-OCT-1999; 99US-0419568.

XX PR 26-OCT-1998; 98US-0178973.

XX PR 16-JUL-1999; 99US-0354243.

XX PA (DUMO/) DUMOUTIER L.

XX PA (LOUA/) LOUAHED J.

XX PA (RENA/) RENAULD J.

XX PI Dumoutier L, Louahed J, Renauld J;

XX WIPI; 2001-638496/73.

XX PT New isolated nucleic acid molecules encoding T cell inducible factors,  
XX useful as markers for expression or effect of interleukin (IL)-9 in a  
XX subject and diagnosing susceptibility to asthma or allergy

XX PS Claim 1; Page 17-19; 26pp; English.

XX CC The invention relates to an isolated nucleic acid molecule, which encodes  
XX a T cell derived inducible factor (TIF) which are upregulated by the

CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor  
CC activation. The TIF proteins (or their mutants) may be used to test IL-9  
CC ant/agonists for their potency against lymphomas, immune system  
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),  
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration  
CC or inhibit differentiation of tissue types in which they are active and  
CC therefore be used to develop treatments for melanomas and hepatomas.  
CC The present sequence a partial genomic sequence for Human TIF.

XX SQ Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;

Query Match 18.5%; Score 207; DB 22; Length 4797;  
Best Local Similarity 100.0%; Pred. No. 9.6e-91;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcgagttagaattgtctgcaatggcgccctgcagaaatctgtgagctcttccctatgg 60

Db 52 tcgagttagaattgtctgcaatggcgccctgcagaaatctgtgagctcttccctatgg 111

Qy 61 ggacctggccaccagctgctccctctcttggccctctgtgtacaggagagcagctg 120

Db 112 ggacctggccaccagctgctccctctcttggccctctgtgtacaggagagcagctg 171

Qy 121 cggccatcagctcccaactgcaggttgacaagtccaactccagcagccctatacaca 180

Db 172 cggccatcagctcccaactgcaggttgacaagtccaactccagcagccctatacaca 231

Qy 181 accgcaccttcagctggctaaggagg 207

Db 232 accgcaccttcagctggctaaggagg 258

## RESULT 12

AAAD09746

ID AAAD09746 standard; cDNA; 778 BP.

XX AC AAAD09746;

XX DT 10-SEP-2001 (first entry)

XX DE Mouse ZCYTO18 cDNA.

XX KW Mouse; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;  
XX cancer; inflammation; gene therapy; ss.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

XX CDS 47..586

XX FT /\*tag= a

XX FT /product= "Mouse ZCYTO18 protein"

XX FT sig\_peptide 47..145

XX FT /\*tag= b

XX FT mat\_peptide 146..583

XX FT /\*tag= c

XX FT /product= "Mouse mature ZCYTO18 protein"

XX WO200146422-A1.

XX PN 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-US35308.

XX PR 23-DEC-1999; 99US-0471767.

XX PR 01-DEC-2000; 2000US-0250841.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Presnell SR, Kindsvogel W;

XX WIPI; 2001-408648/43.

XX DR P-PSDB; AAE05052.

XX Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -  
 PT Example 5; Page 160-162; 167pp; English.  
 PS  
 XX The patent discloses novel human cytokine, ZCYTO18 protein and its  
 CC corresponding DNA. ZCYTO18 protein induces proliferation of cells  
 CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity.  
 CC In K562 cells, ZCYTO18 DNA is useful for detecting a genetic  
 CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful  
 CC for detecting cancer and inflammation. ZCYTO18 protein is useful for  
 CC killing cancer cells. It is useful for increasing platelets in a  
 CC patient or injured tissue. It is also used in gene therapy.  
 CC The present sequence is a cDNA encoding mouse cytokine, ZCYTO18.  
 XX Sequence 778 BP; 213 A; 193 C; 197 G; 175 T; 0 other;  
 SQ

Query Match 3.1%; Score 35; DB 22; Length 778;  
 Best Local Similarity 100.0%; Pred. No. 7e-07;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 acagtgaagcttgagagagtgaggagatcaa 505  
 |||||  
 Db 497 acagtgaagcttgagagagtgaggagatcaa 531  
 |||||

RESULT 13  
 AAA28815  
 ID AAA28815 standard; cDNA; 1119 BP.  
 AC AAA28815;  
 DT 04-SEP-2000 (first entry)  
 XX Murine T cell inducible factor alpha cDNA.  
 XX  
 XX TIF-alpha; T cell derived inducible factor; Interleukin 9; STAT; IL-9;  
 KW Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.  
 KW  
 OS Mus sp.  
 XX Key Location/Qualifiers  
 FH 52..591  
 FT /\*tag= a  
 FT primer\_bind  
 FT primer\_bind  
 FT complement (764..784)  
 FT /\*tag= c  
 FT /\*note= "PCR primer appearing as AAS14861"  
 FT /\*note= "PCR primer appearing as AAS14862"  
 PN WO20024758-A1.  
 XX 04-MAY-2000.  
 PD 18-OCT-1999; 99WO-US24424.  
 XX 26-OCT-1998; 98US-0178973.  
 PR 16-JUL-1999; 99US-0354243.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Dumoutier L, Louhed J, Renauld J;  
 PI WPI; 2000-422495/36.  
 XX P-PSDB; AAY92877.  
 DR New nucleic acid molecule encoding a T cell derived inducible factor  
 XX for treating asthma, an allergy or lymphoma  
 PT Claim 1; Page 33; 46pp; English.  
 PS This cDNA encodes T cell derived inducible factor (TIF) alpha identified  
 CC by subtraction cloning from a murine lymphoma cell line BW5147 in the  
 CC presence or absence of interleukin 9 (IL-9). BW5147, can be grown in  
 CC vitro, without the need to add any cytokines to its culture medium. Many  
 CC IL-9 activities are mediated by activation of STAT transcription  
 CC factors. The novel TIFs were expressed in the presence of IL-9, but not

CC in its absence. TIFs induce STAT activation in cells. They can be used,  
 CC e.g. in the stimulation of regeneration of targeted tissues. Their  
 CC inhibitors or antagonists can be used to retard, prevent or inhibit  
 CC differentiation of other tissues. The TIFs and their coding sequences are  
 CC useful in the treatment of asthma, allergies and lymphoma (claimed). They  
 CC are also useful for identifying compounds that inhibit or activate T cell  
 CC induced factor activity in a cell (claimed).  
 XX Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;  
 SQ

Query Match 3.1%; Score 35; DB 21; Length 1119;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-07;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 acagtgaagcttgagagagtgaggagatcaa 505  
 |||||  
 Db 502 acagtgaagcttgagagagtgaggagatcaa 536  
 |||||

RESULT 14  
 AAS14858  
 ID AAS14858 standard; cDNA; 1119 BP.  
 AC AAS14858;  
 XX 19-DEC-2001 (first entry)  
 XX Mouse cDNA encoding T cell derived inducible factor, TIFalpha.  
 DE  
 XX  
 XX Mouse; T cell derived inducible factor; TIFalpha; ss; anti-allergic;  
 KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;  
 KW cancer; lymphoma; immune system disorder; allergy; asthma;  
 KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;  
 KW thyroiditis; melanoma; hepatoma.  
 XX Mus musculus.  
 OS  
 XX Key Location/Qualifiers  
 FH 52..591  
 FT /\*tag= a  
 FT product= "TIFalpha"  
 FT primer\_bind  
 FT primer\_bind  
 FT primer\_bind  
 FT complement (764..784)  
 FT /\*tag= c  
 FT /\*note= "PCR primer appearing as AAS14861"  
 FT /\*note= "PCR primer appearing as AAS14862"  
 PN US2001024652-A1.  
 XX 27-SEP-2001.  
 PD 29-DEC-2000; 2000US-0751797.  
 XX 18-OCT-1999; 99US-0419568.  
 PR 26-OCT-1998; 98US-0178973.  
 PR 16-JUL-1999; 99US-0354243.  
 XX (DUMO/) DUMOUTIER L.  
 PA (LOUA/) LOUAHED J.  
 PA (RENA/) RENAULD J.  
 XX Dumoutier L, Louahed J, Renauld J;  
 PI WPI; 2001-638496/73.  
 XX P-PSDB; AAU09090.  
 DR New isolated nucleic acid molecules encoding T cell inducible factors,  
 XX useful as markers for expression or effect of interleukin (IL)-9 in a  
 PT subject and diagnosing susceptibility to asthma or allergy -  
 XX Claim 1; Page 10; 26pp; English.  
 PS

XX The invention relates to an isolated nucleic acid molecule, which encodes  
CC a T cell derived inducible factor (TIF) which are upregulated by the  
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor  
CC activation. The TIF proteins (or their mutants) may be used to test IL-9  
CC ant/agonists for their potency against lymphomas, immune system  
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),  
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration  
CC or inhibit differentiation of tissue types in which they are active and  
CC therefore be used to develop treatments for melanomas and hepatomas.  
XX The present sequence encodes mouse Tifalpha.  
XX  
SQ Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;

Query Match 3.1%; Score 35; DB 22; Length 1119;  
Best Local Similarity 100.0%; Pred. No. 7.1e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 acagtgaagaaagcttgagagagtgagagatcaa 505  
|||||  
Db 502 acagtgaagaaagcttgagagagtgagagatcaa 536  
|||||

RESULT 15  
AAC81774  
ID AAC81774 standard; cDNA; 1166 BP.  
XX  
AC AAC81774;  
XX  
DT 23-FEB-2001 (first entry)  
XX  
DE Murine GIL-19 protein coding sequence.  
XX  
KW Mouse; GIL-19/AE289; IL-10; interleukin-10; nutrition;  
KW cell proliferation; immune stimulation; immune suppression;  
KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.  
XX  
OS Mus sp.  
XX  
PN WO200065027-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US11479.  
XX  
PR 28-APR-1999; 99US-0131473.  
XX  
PA (GEM ) GENETICS INST INC.  
XX  
PI Jacobs K, Fouser L, Spaulding V, Xuan D;  
XX  
DR WPI; 2000-687325/67.  
XX  
PT Human GIL-19 protein that shows a high degree of homology to IL  
PT (interleukin)-10, useful in upregulation of humoral immune responses,  
PT as an antiinflammatory agent and as a modulator of immune responses  
PT associated with injury -  
XX  
PS Disclosure; Fig 1; 60pp; English.  
XX  
CC The present invention provides the protein and coding sequences for the  
CC novel human GIL-19/AE289 protein. The protein shows homology to  
CC interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used  
CC in the regulation of cell proliferation and differentiation,  
CC haematopoiesis, immune stimulation or suppression, tissue growth and  
CC tumour inhibition. In addition, it also has uses in the treatment of  
XX inflammation and in nutrition.  
SQ Sequence 1166 BP; 375 A; 241 C; 244 G; 306 T; 0 other;

Query Match 3.1%; Score 35; DB 21; Length 1166;

Best Local Similarity 100.0%; Pred. No. 7.1e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 acagtgaagaaagcttgagagagtgagagatcaa 505  
|||||  
Db 525 acagtgaagaaagcttgagagagtgagagatcaa 559  
|||||

Search completed: September 23, 2002, 02:11:28  
Job time: 5249 sec

us-09-746-375-1.rng

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Mon Sep 23 09:43:52 2002



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 00:51:20 ; Search time 51.77 Seconds  
(without alignments)  
5295.093 Million cell updates/sec

Title: us-09-746-375-1

Perfect score: 1116  
Sequence: 1 tcgagtagaattgtctgca.....ataaacacttgatccta 1116

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 14

Total number of hits satisfying chosen parameters: 1870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/1na/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/1na/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/1na/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/1na/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/1na/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	639	57.3	690	4	US-09-354-243B-24
2	207	18.5	4797	4	US-09-354-243B-25
3	35	3.1	1119	4	US-09-178-973B-7
4	35	3.1	1119	4	US-09-354-243B-7
5	31	2.8	7445	4	US-09-178-973B-8
6	31	2.8	7445	4	US-09-354-243B-8
7	28	2.5	1111	4	US-09-178-973B-9
8	28	2.5	1111	4	US-09-354-243B-9
9	28	2.5	5935	4	US-09-178-973B-17
10	28	2.5	5935	4	US-09-354-243B-29
11	22	2.0	22	4	US-09-354-243B-16
12	21	1.9	21	4	US-09-354-243B-18
13	21	1.9	21	4	US-09-354-243B-19
14	20	1.8	2908	3	US-08-487-799-1
15	20	1.8	22846	2	US-08-469-461-3
16	20	1.8	22846	3	US-07-890-609-3
17	18	1.6	1939	1	US-07-715-751B-2
18	17	1.5	356	4	US-09-319-730-16
19	17	1.5	452	2	US-08-378-235B-4
20	17	1.5	573	2	US-08-290-665A-134
21	17	1.5	573	5	PCT-US95-10398-134
22	17	1.5	1519	1	US-07-971-759-19
23	17	1.5	1628	2	US-08-883-515-3
24	17	1.5	3217	4	US-09-232-200-64
25	17	1.5	3217	4	US-09-232-197-64
26	17	1.5	3217	4	US-09-232-201-64
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28      17      1.5 15378 3 US-08-785-420-1 Sequence 1, Appli
c 29      17      1.5 28804 2 US-08-592-874-1 Sequence 1, Appli
c 30      17      1.5 28804 3 US-09-096-942-2 Sequence 2, Appli
c 31      17      1.5 28804 3 US-09-096-867-2 Sequence 2, Appli
c 32      17      1.5 80161 3 US-09-036-987A-1 Sequence 1, Appli
c 33      17      1.5 80161 4 US-09-370-700-1 Sequence 1, Appli
c 34      17      1.5 246240 2 US-08-724-394A-20 Sequence 20, Appli
c 35      17      1.5 246240 2 US-08-724-394A-21 Sequence 21, Appli
c 36      17      1.5 246240 2 US-08-724-394A-22 Sequence 22, Appli
c 37      16      1.4 77 1 US-08-400-440A-30 Sequence 30, Appli
c 38      16      1.4 77 1 US-08-463-093A-30 Sequence 30, Appli
c 39      16      1.4 77 2 US-08-460-888A-30 Sequence 30, Appli
c 40      16      1.4 77 2 US-08-894-578-30 Sequence 30, Appli
c 41      16      1.4 77 4 US-09-412-017-30 Sequence 30, Appli
c 42      16      1.4 86 2 US-08-525-742-50 Sequence 50, Appli
c 43      16      1.4 201 1 US-08-021-667A-18 Sequence 18, Appli
c 44      16      1.4 201 1 US-08-410-544-18 Sequence 18, Appli
c 45      16      1.4 201 1 US-08-728-785A-18 Sequence 18, Appli

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#### ALIGNMENTS

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RESULT 1
US-09-354-243B-24
; Sequence 24, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louheid, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; TITLE OF INVENTION: (TIFS)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 24
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-24

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Query Match 57.3%; Score 639; DB 4; Length 690;  
Best Local Similarity 100.0%; Pred. No. 5e-302;  
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 tcgagttagaattgtctgcaatggccgccttcgacagaatactgtgagctctttcctattgg 60
Db 52 tcgagttagaattgtctgcaatggccgccttcgacagaatactgtgagctctttcctattgg 111
QY 61 ggaccttgagccacagctgcctcctctcttgcctcttgcctcttgcctgagggagagcagctg 120
Db 112 ggaccttgagccacagctgcctcctcctcttgcctcttgcctcttgcctgagggagagcagctg 171
QY 121 cgcccatcagctcccaactgcagggcttgacaagtcacaaactccagcagccctatacacca 180
Db 172 cgcccatcagctcccaactgcagggcttgacaagtcacaaactccagcagccctatacacca 231
QY 181 accgacacttcagctgctgctgaaggaggtagcttagctgataaacacacagacgttcgtc 240
Db 232 accgacacttcagctgctgctgaaggaggtagcttagctgataaacacacagacgttcgtc 291
QY 241 tcattggggagaaaactgttcacacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
Db 292 tcattggggagaaaactgttcacacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 351
QY 301 aggtgctgaacttcaccccttgagaagtgctgttccctcaatctgatagtgttccacgctt 360

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Db 352 aggtgtaactcacccttgaaagagtgtcttccctcaatctgataggtccagcctt 411  
Qy 361 atatcaggagggtggtgccccttctctgcccaggtccagcaacaggctaaagcacatgtcata 420  
Db 412 atatgcaggagggtggtgccccttctctgcccaggtccagcaacaggctaaagcacatgtcata 471  
Qy 421 ttgaaggtgatgacctgcatactacagagggaatgtgcacaaagctgaaggacacagtgaaaa 480  
Db 472 ttgaaggtgatgacctgcatactacagagggaatgtgcacaaagctgaaggacacagtgaaaa 531  
Qy 481 agcttgagagagtgagagagatcaaaagcaattggagaactggattgtctttatgtctc 540  
Db 532 agcttgagagagtgagagagatcaaaagcaattggagaactggattgtctttatgtctc 591  
Qy 541 tgagaaatgctgtcatttgccagagcaaaagctgaaaaatgaataaaccctcttcc 600  
Db 592 tgagaaatgctgtcatttgccagagcaaaagctgaaaaatgaataaaccctcttcc 651  
Qy 601 ctgctagaataacaattagatgccccaagcgattttt 639  
Db 652 ctgctagaataacaattagatgccccaagcgattttt 690  
RESULT 2  
US-09-354-243B-25  
; Sequence 25, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa  
; TITLE OF INVENTION: (Tifs)  
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 25  
; LENGTH: 4797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-354-243B-25  
Query Match 18.5%; Score 207; DB 4; Length 4797;  
Best Local Similarity 100.0%; Pred. No. 1.6e-91;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 tcagattagaattgtctgcaatgcccgccttcgagaaatctgtgagctcttctccattgg 60  
Db 52 tcagattagaattgtctgcaatgcccgccttcgagaaatctgtgagctcttctccattgg 111  
Qy 61 ggaacctggccacagctgctctctctcttggccctcttggtacaggaggagcagctg 120  
Db 112 ggaacctggccacagctgctctctctcttggccctcttggtacaggaggagcagctg 171  
Qy 121 cgccatcagctcccaactgcaggcttgcaagtgcccaacttcacagcagccctatatcaca 180  
Db 172 cgccatcagctcccaactgcaggcttgcaagtgcccaacttcacagcagccctatatcaca 231  
Qy 181 accgacattcatgctgctgaaggagg 207  
Db 232 accgacattcatgctgctgaaggagg 258  
RESULT 3  
US-09-178-973B-7  
; Sequence 7, Application US/09178973B

; Patent No. 6274710  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Renauld, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible  
; TITLE OF INVENTION: (Tifs)  
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
; FILE REFERENCE: LUD 5543  
; CURRENT APPLICATION NUMBER: US/09/178,973B  
; CURRENT FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 7  
; LENGTH: 1119  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-178-973B-7  
Query Match 3.1%; Score 35; DB 4; Length 1119;  
Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 471 acagtgaagagcttgagagagtgaggagatcaa 505  
Db 502 acagtgaagagcttgagagagtgaggagatcaa 536  
RESULT 4  
US-09-354-243B-7  
; Sequence 7, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Renauld, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible  
; TITLE OF INVENTION: (Tifs)  
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 7  
; LENGTH: 1119  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
US-09-354-243B-7  
Query Match 3.1%; Score 35; DB 4; Length 1119;  
Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 471 acagtgaagagcttgagagagtgaggagatcaa 505  
Db 502 acagtgaagagcttgagagagtgaggagatcaa 536  
RESULT 5  
US-09-178-973B-8  
; Sequence 8, Application US/09178973B  
; Patent No. 6274710  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Renauld, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible  
; TITLE OF INVENTION: (Tifs)  
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof

FILE REFERENCE: LUD 5543  
CURRENT APPLICATION NUMBER: US/09/178,973B  
CURRENT FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO 8  
LENGTH: 7445  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-178-973B-8

Query Match 2.8%; Score 31; DB 4; Length 7445;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 ttatttaaatggtattttatttagaaacat 1011  
|||||  
DB 7008 ttatttaaatggtattttatttagaaacat 7038

RESULT 6  
US-09-354-243B-8  
Sequence 8, Application US/09354243B  
Patent No. 6359117  
GENERAL INFORMATION:  
APPLICANT: Dumoutier, Laure  
APPLICANT: Louhed, Jamila  
APPLICANT: Renauld, Jean-Christophe  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa  
TITLE OF INVENTION: (TIFS)  
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
FILE REFERENCE: LUD 5543.1  
CURRENT APPLICATION NUMBER: US/09/354,243B  
CURRENT FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US09/178,973  
PRIOR FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 29  
SEQ ID NO 8  
LENGTH: 7445  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
US-09-354-243B-8

Query Match 2.8%; Score 31; DB 4; Length 7445;  
Best Local Similarity 100.0%; Pred. No. 8.9e-06;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 ttatttaaatggtattttatttagaaacat 1011  
|||||  
DB 7008 ttatttaaatggtattttatttagaaacat 7038

RESULT 7  
US-09-178-973B-9  
Sequence 9, Application US/09178973B  
Patent No. 6274710  
GENERAL INFORMATION:  
APPLICANT: Dumoutier, Laure  
APPLICANT: Louhed, Jamila  
APPLICANT: Renauld, Jean-Christophe  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac  
TITLE OF INVENTION: (TIFS)  
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
FILE REFERENCE: LUD 5543  
CURRENT APPLICATION NUMBER: US/09/178,973B  
CURRENT FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO 9  
LENGTH: 1111  
TYPE: DNA  
ORGANISM: Mus musculus

US-09-178-973B-9

Query Match 2.5%; Score 28; DB 4; Length 1111;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 ttatttaaatggtattttatttagaaaa 1008  
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DB 981 ttatttaaatggtattttatttagaaaa 1008

RESULT 8  
US-09-354-243B-9  
Sequence 9, Application US/09354243B  
Patent No. 6359117  
GENERAL INFORMATION:  
APPLICANT: Dumoutier, Laure  
APPLICANT: Louhed, Jamila  
APPLICANT: Renauld, Jean-Christophe  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible  
TITLE OF INVENTION: (TIFS)  
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
FILE REFERENCE: LUD 5543.1  
CURRENT APPLICATION NUMBER: US/09/354,243B  
CURRENT FILING DATE: 1999-07-16  
PRIOR APPLICATION NUMBER: US09/178,973  
PRIOR FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 29  
SEQ ID NO 9  
LENGTH: 1111  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
US-09-354-243B-9

Query Match 2.5%; Score 28; DB 4; Length 1111;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 ttatttaaatggtattttatttagaaaa 1008  
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DB 981 ttatttaaatggtattttatttagaaaa 1008

RESULT 9  
US-09-178-973B-17  
Sequence 17, Application US/09178973B  
Patent No. 6274710  
GENERAL INFORMATION:  
APPLICANT: Dumoutier, Laure  
APPLICANT: Louhed, Jamila  
APPLICANT: Renauld, Jean-Christophe  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible  
TITLE OF INVENTION: (TIFS)  
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
FILE REFERENCE: LUD 5543  
CURRENT APPLICATION NUMBER: US/09/178,973B  
CURRENT FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO 17  
LENGTH: 5935  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-178-973B-17

Query Match 2.5%; Score 28; DB 4; Length 5935;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 ttatttaaatggtattttatttagaaaa 1008

Db 5694 tttattaataggattattattagaaa 5721  
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RESULT 10  
US-09-354-243B-29  
; Sequence 29, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides (TIFs)  
; TITLE OF INVENTION: (TIFs)  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US09/178,973  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 29  
; LENGTH: 5935  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-354-243B-29

Query Match 2.5%; Score 28; DB 4; Length 5935;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 981 tttattaataggattattattagaaa 1008  
|||||

Db 5694 tttattaataggattattattagaaa 5721  
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RESULT 11  
US-09-354-243B-16/c  
; Sequence 16, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides (TIFs)  
; TITLE OF INVENTION: (TIFs)  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US09/178,973  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 16  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-354-243B-16

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Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 475 tgaataaaccttgagagagtg 496  
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Db 22 TCAAAAAGCTTGAGAGAGTGG 1

US-09-354-243B-18/c  
; Sequence 18, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides (TIFs)  
; TITLE OF INVENTION: (TIFs)  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US09/178,973  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 18  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-354-243B-18

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Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AGTGTGCTCTCTCTGCCA 1  
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RESULT 13  
US-09-354-243B-19/c  
; Sequence 19, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides (TIFs)  
; TITLE OF INVENTION: (TIFs)  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US09/178,973  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-354-243B-19

Query Match 1.9%; Score 21; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 agtggtgacctctctgcca 390  
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Db 21 AGTGTGCTCTCTCTGCCA 1  
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RESULT 14  
US-08-487-799-1  
; Sequence 1, Application US/08487799C  
; Patent No. 6010908  
; GENERAL INFORMATION:  
; APPLICANT: Gruenert, Dieter C.

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; APPLICANT: Kunzelmann, Karl
; TITLE OF INVENTION: GENE THERAPY BY SMALL FRAGMENTS HOMOLOGOUS REPLACEMENT
; FILE REFERENCE: 480.18-1(HV)
; CURRENT APPLICATION NUMBER: US/08/487,799C
; CURRENT FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 07/933,471
; EARLIER FILING DATE: 1992-08-21
; EARLIER APPLICATION NUMBER: 08/409,544
; EARLIER FILING DATE: 1995-03-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: human
US-08-487-799-1

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Query Match      1.8%; Score 20; DB 3; Length 2908;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 822 caattattttttaataat 841
Db 1453 caattattttttaataat 1472

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RESULT 15
US-08-469-461-3
; Sequence 3, Application US/08/469461B
; Patent No. 5981178
; GENERAL INFORMATION:
; APPLICANT: Tsui, Lap-Chee
; APPLICANT: Rommins, Johanna M.
; APPLICANT: Kerem, Bat-Sheva
; TITLE OF INVENTION: Introns and Exons of the Cystic Fibrosis Gene and
; FILE REFERENCE: 3477-61, 033477/139840
; CURRENT APPLICATION NUMBER: US/08/469,461B
; CURRENT FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 22846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-469-461-3

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Query Match      1.8%; Score 20; DB 2; Length 22846;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 822 caattattttttaataat 841
Db 9242 caattattttttaataat 9261

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-09-746-375-1  
Perfect score: 1116  
Sequence: 1 tcgagtagaattctgca.....ataaacacttgatattccta 1116

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

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Total number of hits satisfying chosen parameters: 158874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: em\_esthum:\*  
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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	28	2.5	256	AV030414	AV030414 AV030414
C 3	28	2.5	700	AK005228	AK005228 Mus muscu
C 4	23	2.1	116	B1314237	B1314237 dai33ci2
C 5	22	2.0	381	B1341427	B1341427 368848 MA
C 6	22	2.0	431	B1341431	B1341431 368853 MA
C 7	22	2.0	446	A2167394	A2167394 SP_00098_A
C 8	22	2.0	718	A0780852	A0780852 HS_3113_B
C 9	21	1.9	182	W21516	W21516 zbs1g10.r1
C 10	21	1.9	192	W21016	W21016 zbs0f12.r1
C 11	21	1.9	210	AA341708	AA341708 EST47366
C 12	21	1.9	234	AA334932	AA334932 EST39303
C 13	21	1.9	240	AW486359	AW486359 72999 MAR
C 14	21	1.9	251	W05048	W05048 za78g02.r1
C 15	21	1.9	262	AA331022	AA331022 EST34794
C 16	21	1.9	295	AV097026	AV097026 AV097026
C 17	21	1.9	301	BF827895	BF827895 RCO-HN002

C 18	1.9	304	10	F00991	F00991 HSB89H092 S
C 19	1.9	305	9	AA486360	AA486360 73004 MAR
C 20	1.9	315	9	AA346165	AA346165 EST52274
C 21	1.9	327	10	BF827890	BF827890 RCO-HN002
C 22	1.9	335	9	AA328929	AA328929 EST32477
C 23	1.9	378	9	AA112190	AA112190 zhs60d07.r
C 24	1.9	384	12	AZ223713	AZ223713 RPI-23-5
C 25	1.9	391	9	AA180126	AA180126 zp34c02.r
C 26	1.9	401	9	AA194504	AA194504 zg06f07.r
C 27	1.9	401	9	AA346264	AA346264 EST52401
C 28	1.9	422	10	BM276287	BM276287 PFEST0aa7
C 29	1.9	429	10	W88590	W88590 zh70h12.r1
C 30	1.9	433	9	AA192403	AA192403 zq01a01.r
C 31	1.9	458	9	AA182400	AA182400 zp16g01.r
C 32	1.9	464	9	AA196108	AA196108 zp99e07.r
C 33	1.9	473	10	BM276043	BM276043 PFEST0aa6
C 34	1.9	476	12	AQ203627	AQ203627 HS_3103_B
C 35	1.9	478	12	AQ664172	AQ664172 HS_5493_B
C 36	1.9	479	9	AW104304	AW104304 xdt7a10.x
C 37	1.9	480	10	W93616	W93616 zd95c04.r1
C 38	1.9	503	12	AZ478642	AZ478642 IM0298C23
C 39	1.9	507	12	AQ992968	AQ992968 RPI-23-3
C 40	1.9	529	10	B1816005	B1816005 PFEST0aa3
C 41	1.9	545	10	BM276174	BM276174 PFEST0aa7
C 42	1.9	548	10	BM275812	BM275812 PFEST0aa8
C 43	1.9	549	10	BM275687	BM275687 PFEST0aa5
C 44	1.9	551	10	BM275051	BM275051 PFEST0aa7
C 45	1.9	555	10	BM274386	BM274386 PFEST0aa4

ALIGNMENTS

RESULT 1  
AQ104025/c  
LOCUS  
DEFINITION  
HS\_3108\_B1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.  
ACCESSION  
AQ104025  
VERSION  
AQ104025.1 GI:3478961  
KEYWORDS  
GSS.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 389)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,K., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
TITLE  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
JOURNAL  
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
MEDLINE  
99380589  
COMMENT  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 3108 row: F column: 1  
Class: BAC ends  
High quality sequence stop: 389.  
Location/Qualifiers  
1. 389  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="plate=3108 Col=1 Row=F"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

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BASE COUNT      119 a      86 c      65 g      118 t      1 others
ORIGIN

Query Match      5.9%; Score 66; DB 12; Length 389;
Best Local Similarity 100.0%; Pred. No. 2.5e-21;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 catattgaagtgatccctgcattccaggagaaatgtgcaaaagctggaaggacacagt 476
|||||
Db 144 CATATTGAAGTGATGACCTGCATATCCAGAGGANTGTGCAAAAGCTGAAGGACACAGT 85

QY 477 aaaaag 482
|||||
Db 84 AAAAAG 79

RESULT 2
AV030414      256 bp      mRNA      linear      EST 31-AUG-1999
LOCUS
DEFINITION
AV030414 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA
clone 1500012D04, mRNA sequence.
ACCESSION
AV030414
VERSION
AV030414.1 GI:4829962
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 256)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara
Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N.,
Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermolabile and thermostable enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
Location/Qualifiers
source
1. .256
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="1500012D04"
/clone_lib="Mus musculus adult C57BL/6J cerebellum"
/sex="male"
/tissue_type="cerebellum"
/dev_stage="adult"
88 a 29 c 41 g 98 t

BASE COUNT      88 a      29 c      41 g      98 t
ORIGIN

Query Match      2.5%; Score 28; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 981 ttatttaaatggattattattatagaaa 1008
|||||
Db 131 TTTATTAAATGCGATTATTATTATAGAAA 158

RESULT 3
AK005228      700 bp      mRNA      linear      HTC 19-JAN-2002
LOCUS
DEFINITION
AK005228 Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
library, clone:1500012D04:Interleukin 10-related T cell-derived
inducible factor, full insert sequence.
ACCESSION
AK005228
VERSION
AK005228.1 GI:12837639
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (strain:C57BL/6J) adult male cerebellum cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:1500012D04.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (sites)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
99279253
MEDLINE
10349636
PUBMED
2 (sites)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 (sites)
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 700)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,
Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yamanaka, I.,
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
Hayashizaki, Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,

```



```

FEATURES
  source              Location/Qualifiers
1..116
  /organism="Xenopus laevis"
  /db_xref="taxon:8355"
  /clone="IMAGE:4963582"
  /clone_lib="NICHD XCC Spl"
  /dev_stage="adult"
  /lab_host="DH10B (phage-resistant)"
  /note="Organ: spleen; Vector: pCMV-SPORT6; Site_1: NotI;
  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
  Average insert size 2.4 kb. Constructed by Life
  Technologies."
BASE COUNT          36 a      17 c      13 g      50 t
ORIGIN

Query Match                2.1%   Score 23;   DB 10;   Length 116;
Best Local Similarity      100.0%;   Pred. No. 4.6;
Matches 23; Conservative  0; Mismatches 0; Indels 0; Gaps 0;

Qy  934  ataaatgattattattattatt 956
|||||
Db    5  ATAAATGATTATTATTATTAT 27

RESULT  5
BI341427/c
LOCUS   BI341427                381 bp    mRNA    linear    EST 30-JUL-2001
DEFINITION  36848 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  BI341427
VERSION    BI341427.1   GI:15034716
KEYWORDS   EST.
SOURCE     pig.
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 381)
AUTHORS   Fahrenkrug,S.C., Frenking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
JOURNAL   Unpublished (2000)
COMMENT   Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCGTATGACCAT
BACKWARD: GTTTCACGACGACG
Plate: 108 row: D column: 15
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
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1..381
  /organism="Sus scrofa"
  /db_xref="taxon:9823"
  /clone_lib="MARC 2P1G"
  /tissue_type="pooled"
  /lab_host="DH10B"
  /note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
  Library made from pooled tissue from testis, ovary,
  endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT          157 a      42 c      58 g      114 t
ORIGIN

Query Match                2.0%   Score 22;   DB 10;   Length 381;
Best Local Similarity      100.0%;   Pred. No. 12.

```

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 829 ttttttaataattgtcttttt 850  
 |||||||  
 Db 29 TTTTAAATAATGCTTTT 8

RESULT 6  
 BI341431/c  
 LOCUS 431 bp mRNA linear EST 30-JUL-2001  
 DEFINITION 368853 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.  
 ACCESSION BI341431  
 VERSION BI341431.1 GI:15034720  
 KEYWORDS EST.  
 SOURCE pig.  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 431)  
 REFERENCE Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,  
 AUTHORS Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.  
 and Keele,J.W.  
 TITLE Design and use of two pooled tissue normalized cDNA libraries for  
 EST discovery in swine  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@mail.marc.usda.gov  
 Single pass sequencing. Bases called and alt.trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
 and -minmatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCACGACG  
 Plate: 108 row: E column: 14  
 Seq primer: ATTTAGTGACACTATAG.  
 FEATURES  
 Location/Qualifiers  
 1..431  
 /organism="Sus scrofa"  
 /db\_xref="taxon:9823"  
 /clone\_lib="MARC 2P1G"  
 /tissue\_type="pooled"  
 /lab\_host="DH10b"  
 /note="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;  
 Library made from pooled tissue from testis, ovary,  
 endometrium, hypothalamus, pituitary, and placenta."  
 BASE COUNT 177 a 51 c 93 g 109 t  
 ORIGIN

Query Match 2.0%; Score 22; DB 10; Length 431;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 829 ttttttaataattgtcttttt 850  
 |||||||  
 Db 239 TTTTAAATAATGCTTTT 218

RESULT 7  
 AZ167394/c  
 LOCUS 446 bp DNA linear GSS 29-AUG-2000  
 DEFINITION SP\_0098\_A2\_A12.SP6E Strongylocentrotus purpuratus, purple sea  
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus  
 genomic clone Plate=98 Col=24 Row=A, DNA sequence.  
 ACCESSION AZ167394  
 VERSION AZ167394.1 GI:8337762  
 KEYWORDS GSS.  
 SOURCE Strongylocentrotus purpuratus.  
 ORGANISM Strongylocentrotus purpuratus

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Echinoidea; Euechinoidea; Echinacea; Echinoida;  
 Strongylocentrotidae; Strongylocentrotus.  
 1 (bases 1 to 446)  
 REFERENCE Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,  
 AUTHORS Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray  
 ,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and  
 Hood,L.  
 TITLE A sea urchin genome project: Sequence scan, virtual map, and  
 additional resources  
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)  
 MEDLINE 20402566  
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L  
 Division of Biology 156-29  
 California Institute of Technology  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 98 row: A column: 24  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 446.  
 FEATURES  
 Location/Qualifiers  
 1..446  
 /organism="Strongylocentrotus purpuratus"  
 /db\_xref="taxon:7668"  
 /clone="Plate=98 Col=24 Row=A"  
 /clone\_lib="Strongylocentrotus purpuratus, purple sea  
 urchin, sperm genomic BAC library"  
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli  
 DH10b"  
 BASE COUNT 169 a 89 c 92 g 96 t  
 ORIGIN

Query Match 2.0%; Score 22; DB 12; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 929 tattataaatgtattattat 950  
 |||||||  
 Db 143 TATTATAAATGTATTATTAT 122

RESULT 8  
 AQ780852  
 LOCUS 718 bp DNA linear GSS 02-AUG-1999  
 DEFINITION HS\_3113\_B1\_B02\_T7C CIT Approved Human Genomic Sperm Library D Homo  
 sapiens genomic clone Plate=3113 Col=3 Row=D, DNA sequence.  
 ACCESSION AQ780852  
 VERSION AQ780852.1 GI:5683812  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 718)  
 REFERENCE Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 AUTHORS Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: <http://www.htsc.washington.edu>  
 Plate: 3113 row: D column: 3  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 718.

#### FEATURES

Location/Qualifiers  
 1..718  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="plate-3113 Col=3 Row=D"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /sex="male"  
 /note="Organ: sperm; Vector: pBelOAC11; BAC Clones in:  
 E-Coli DH10B"  
 201 a 161 c 150 g 204 t 2 others

#### BASE COUNT

ORIGIN  
 Query Match 2.0%; Score 22; DB 12; Length 718;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 776 ttattgataacatttcattgt 797

Db 87 TTTATTGATACATTTCATTGT 108

#### RESULT

W21516/c  
 LOCUS  
 DEFINITION  
 W21516 182 bp mRNA linear EST 20-AUG-1996  
 IMAGE:307146 5' similar to gb:Z15030\_rnal MYOSIN REGULATORY LIGHT  
 CHAIN 2, VENTRICULAR (HUMAN);, mRNA sequence.  
 W21516  
 W21516.1 GI:1298157  
 EST.  
 SOURCE  
 human.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 182)  
 AUTHORS  
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins  
 , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore  
 , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,  
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)  
 97044478

#### TITLE

JOURNAL  
 MEDLINE  
 COMMENT  
 Contact: Wilton RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
 Insert Length: 658 Std Error: 0.00  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 168.  
 Location/Qualifiers  
 1..182  
 /organism="Homo sapiens"  
 /db\_xref="GDB:1250558"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:307146"  
 /clone\_lib="Soares\_fetal\_lung\_NbHL19W"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer

#### FEATURES

Location/Qualifiers  
 1..182  
 /organism="Homo sapiens"  
 /db\_xref="GDB:1250558"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:307146"  
 /clone\_lib="Soares\_fetal\_lung\_NbHL19W"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTCAAGTGGAGCGCGCAATTTTTTTTTTTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo. This library was constructed  
 from the same fetus as the fetal heart library, Soares  
 fetal heart NbHL19W."

BASE COUNT 51 a 47 c 52 g 30 t 2 others  
 ORIGIN

Query Match 1.9%; Score 21; DB 10; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 tctctctctggccctctgtg 102

Db 34 TCCTTCTCTGGCCCTCTGG 14

#### RESULT

W21016/c  
 LOCUS  
 DEFINITION  
 W21016 192 bp mRNA linear EST 20-AUG-1996  
 IMAGE:307055 5' similar to gb:L03785 MYOSIN REGULATORY LIGHT CHAIN  
 5 (HUMAN);, mRNA sequence.  
 W21016  
 W21016.1 GI:1297912  
 EST.  
 KEYWORDS  
 SOURCE  
 human.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 192)  
 AUTHORS  
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins  
 , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore  
 , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,  
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)  
 97044478

#### TITLE

JOURNAL  
 MEDLINE  
 COMMENT  
 Contact: Wilton RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
 Insert Length: 685 Std Error: 0.00  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 166.  
 Location/Qualifiers  
 1..192  
 /organism="Homo sapiens"  
 /db\_xref="GDB:1250467"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:307055"  
 /clone\_lib="Soares\_fetal\_lung\_NbHL19W"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer  
 [5'-TGTTACCAATCTCAAGTGGAGCGCGCAATTTTTTTTTTTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of

#### FEATURES

Location/Qualifiers  
 1..192  
 /organism="Homo sapiens"  
 /db\_xref="GDB:1250467"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:307055"  
 /clone\_lib="Soares\_fetal\_lung\_NbHL19W"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer  
 [5'-TGTTACCAATCTCAAGTGGAGCGCGCAATTTTTTTTTTTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bênto Soares and M.Fátima Bonaído. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbhH19W."

BASE COUNT 53 a 53 c 51 g 34 t 1 others  
ORIGIN

Query Match 1.9%; Score 21; DB 10; Length 192;

Best Local Similarity 100.0%; Pred. No. 41; Mismatches 0; Indels 0; Gaps 0;

QY 82 tcctctcttggccctcttgg 102  
|||||

Db 59 TCCTCTCTTGGCCCTCTTGG 39

RESULT 11

AA341708/c

LOCUS EST21-APR-1997  
DEFINITION 210 bp mRNA linear EST 21-APR-1997  
to myosin light chain 2, mRNA sequence.

ACCESSION

AA341708

VERSION

AA341708.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 210)

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White

, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Snall, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferlie, A., Fischer, C., Hastings, G.A., He, W.W.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kosak, D.L.,

Kunsch, C., Hung, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and

Venter, J.C.

TITLE

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL

96026280

MEDLINE

COMMENT

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Location/Qualifiers

1. 210

/organism="Homo sapiens"

/db\_xref="ATCC (inhost):143553"

/db\_xref="taxon:9606"

/clone\_lib="Fetal muscle"

/tissue\_type="muscle"

/dev\_stage="fetus, 24 wks"

/note="vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:

XhoI"

BASE COUNT 55 a 56 c 61 g 34 t 4 others

ORIGIN

Query Match 1.9%; Score 21; DB 9; Length 210;

Best Local Similarity 100.0%; Pred. No. 41; Mismatches 0; Indels 0; Gaps 0;

QY 82 tcctctcttggccctcttgg 102  
|||||

Db 62 TCCTCTCTTGGCCCTCTTGG 42

RESULT 12

AA334932/c

LOCUS

DEFINITION

234 bp mRNA linear

EST21-APR-1997

to myosin light chain-2, type I, mRNA sequence.

ACCESSION

AA334932

VERSION

AA334932.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 234)

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White

, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Snall, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferlie, A., Fischer, C., Hastings, G.A., He, W.W.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kosak, D.L.,

Kunsch, C., Hung, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L.,

Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon

, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and

Venter, J.C.

TITLE

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL

96026280

MEDLINE

COMMENT

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Location/Qualifiers

1. 234

/organism="Homo sapiens"

/db\_xref="ATCC (inhost):136696"

/db\_xref="taxon:9606"

/clone\_lib="Embryo, 9 week"

/dev\_stage="embryo, 9 wks"

/note="vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:

XhoI"

BASE COUNT 62 a 62 c 69 g 39 t 2 others

QY 82 tcctctcttgccctcttgg 102  
|||||  
Db 61 tcctctcttgccctcttgg 41

RESULT 13  
AW486359 240 bp mRNA linear EST 25-APR-2001  
DEFINITION 72999 MARC lBOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION AW486359  
VERSION AW486359.1 GI:7056465  
KEYWORDS EST.  
SOURCE COW.  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 240)  
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W., Rohrer,G.A., Chitko-McKown,C.G.,  
Perteau,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and  
Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013

COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.980504 e. Vector identified by cross\_match with the -minscore 20  
and -minmatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCAGCAGC  
Plate: 33 row: G column: 10  
Seq primer: ATTTAGGTGACACTATAG.

FEATURES  
source  
1..240  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC lBOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"

/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from lymph node, ovary,  
fat, hypothalamus, and pituitary."  
BASE COUNT 60 a 33 g 108 t  
ORIGIN

Query Match 1.9%; Score 21; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 934 ataatgtattattattatt 954  
|||||  
Db 30 ATAAATGTATTATTATTATT 50

RESULT 14  
W05048/c 251 bp mRNA linear EST 23-APR-1996  
LOCUS za78902.r1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:298706 5' similar to gb:215030 rnal MYOSIN REGULATORY LIGHT  
CHAIN 2, VENTRICULAR (HUMAN);, mRNA sequence.  
ACCESSION W05048  
VERSION W05048.1 GI:1277978

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL

COMMENT

FEATURES  
source

1..251  
/organism="Homo sapiens"  
/db\_xref="GDB:1243630"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:298706"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer  
15'-NGTACCAATCTGAGTGAGCGGCCCAATTTTTTTTTTTT-3',  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NbHL19W."

BASE COUNT 72 a 59 c 70 g 45 t 5 others

ORIGIN

Query Match 1.9%; Score 21; DB 10; Length 251;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 tcctctcttgccctcttgg 102  
|||||

Db 43 TCCTCTCTTGCCCTCTTGG 23

RESULT 15  
AA331022/c 262 bp mRNA linear EST 21-APR-1997

LOCUS EST34794 Embryo, 6 week I Homo sapiens cDNA 5' end similar to

DEFINITION similar to myosin 2, light chain, type I, mRNA sequence.

ACCESSION AA331022

VERSION AA331022.1 GI:1983264

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 262)

AUTHORS Adams,M.D., Kervage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult  
C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White  
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,  
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 251)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston  
R., Williamson,A., Wohlmann,P. and Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: mob.REGA+ET  
High quality sequence stop: 176.

FEATURES  
Location/Qualifiers

1..251  
/organism="Homo sapiens"  
/db\_xref="GDB:1243630"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:298706"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer  
15'-NGTACCAATCTGAGTGAGCGGCCCAATTTTTTTTTTTT-3',  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NbHL19W."

BASE COUNT 72 a 59 c 70 g 45 t 5 others

ORIGIN

Query Match 1.9%; Score 21; DB 10; Length 251;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 tcctctcttgccctcttgg 102  
|||||

Db 43 TCCTCTCTTGCCCTCTTGG 23

RESULT 15  
AA331022/c 262 bp mRNA linear EST 21-APR-1997

LOCUS EST34794 Embryo, 6 week I Homo sapiens cDNA 5' end similar to

DEFINITION similar to myosin 2, light chain, type I, mRNA sequence.

ACCESSION AA331022

VERSION AA331022.1 GI:1983264

KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 262)

AUTHORS Adams,M.D., Kervage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult  
C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White  
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,  
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnelm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weisner, P.S., Olsen, H., Raymond, L., Wei, F.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1. .262

/organism="Homo sapiens"

/db\_xref="ATCC (inhost):132654"

/db\_xref="taxon:9606"

/clone\_lib="Embryo, 6 week I"

/dev\_stage="embryo, 6 wks"

/note="Organ: embryo; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"

70 a 68 c 73 g 50 t 1 others

BASE COUNT

ORIGIN

Query Match 1.9%; Score 21; DB 9; Length 262;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 82 tccttctcttgccctcttg 102

Db 29 TCCTTCTCTTGCCCTCTTGG 9

Search completed: September 23, 2002, 02:07:33

Job time: 5129 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:31:39 ; Search time 2227.14 Seconds  
(without alignments)  
10486.101 Million cell updates/sec

Title: us-09-746-375-1

Perfect score: 1116  
Sequence: 1 tcagagtagaattgtctga.....ataaacacttgatataccta 1116

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_hgt\_hum.\*
- 31: em\_hgt\_inv.\*
- 32: em\_hgt\_other.\*
- 33: em\_hgtgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1116	100.0	1116	6	AX151713	Sequence
2	1116	100.0	1116	6	AX179578	Sequence
3	1114.4	99.9	1167	9	AF279437	Homo sapi
4	1114	99.8	1152	6	AX092422	Sequence
5	1096.6	98.3	1139	6	AX054620	Sequence
6	1090.4	97.7	1132	6	AX048204	Sequence
7	639	57.3	690	9	HS277247	Homo sapi
8	636.4	57.0	8393	9	AF387519	Homo sapi
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11	564	50.5	135146	2	AC087562	Pan trogl
12	525.2	47.1	1111	6	AR165228	Sequence
13	525.2	47.1	1118	10	MMU249492	Mus muscu
14	524.4	47.0	1119	6	AR165226	Sequence
15	524.4	47.0	1121	10	MMU249491	Mus muscu
16	429.2	38.5	778	6	AX179614	Sequence
17	380	34.1	537	6	AX054622	Sequence
18	356.4	31.9	501	6	AX179581	Sequence
19	216.4	19.4	5935	6	AR165234	Sequence
20	216.4	19.4	5935	10	MMU294728	Mus muscu
21	215.6	19.3	7445	6	AR165227	Sequence
22	215.6	19.3	8270	10	MMU294727	Mus muscu
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ALIGNMENTS

RESULT 1  
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LOCUS AX151713 1116 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 14 from Patent WO0140467.  
ACCESSION AX151713  
VERSION AX151713.1 GI:14533647  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1116)  
AUTHORS Presnell,S.R., Xu,W., Kindsvogel,W. and Chen,Z.  
TITLE Human cytokine receptor  
JOURNAL Patent: WO 0140467-A 14 07-JUN-2001;  
ZymoGenetics, Inc. (US)  
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source location/Qualifiers  
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BASE COUNT 336 a 229 c 222 g 329 t  
ORIGIN

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Matches 1116; Conservative 0; Mismatches 0;

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RESULT 2  
AX179578 AX179578 1116 bp DNA linear PAT 06-AUG-2001  
LOCUS Sequence 1 from Patent WO0146422.  
DEFINITION  
ACCESSION AX179578  
VERSION AX179578.1 GI:15132010  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1116)  
Presnell, S.R. and Kindsvogel, W.  
AUTHORS  
Cytokine zcyto18  
TITLE  
JOURNAL Patent: WO 0146422-A 1 28-JUN-2001;  
ZymoGenetics, Inc. (US)  
FEATURES  
Location/Qualifiers  
1..1116  
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BASE COUNT 336 a 229 c 222 g 329 t  
ORIGIN

Query Match 100.0%; Score 1116; DB 6; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 1.7e-211;  
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 153 from Patent WO0116318.
ACCESSION AX092422
VERSION AX092422.1 GI:13444525
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 153 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.3e-211;
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RESULT 5
AX054620
LOCUS AX054620 1139 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 1 from Patent WO0073457.
ACCESSION AX054620
VERSION AX054620.1 GI:12228184
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Parham,C.B., de waal Malefyt,R. and Marehalli,N.L.
TITLE Mammalian interleukin-10 homologs: il-d110 and il-d210
JOURNAL Patent: WO 0073457-A 1 07-DEC-2000;
SCHERING CORPORATION (US)
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Query Match 98.3%; Score 1096.6; DB 6; Length 1139;
Best Local Similarity 99.5%; Pred. NO. 1.2e-207;
Matches 1096; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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RESULT 6
LOCUS AX048204 1132 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 44 from Patent WO0070049.
ACCESSION AX048204
VERSION AX048204.1 GI:11876994
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
Azimzai,Y., Lu,D.A. and Patterson,C.
TITLE Extracellular signaling molecules
JOURNAL Patent: WO 0070049-A 44 23-NOV-2000;
Incyte Genomics, Inc. (US)
FEATURES
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1..1132
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 5571181CBI"
BASE COUNT 333 a 240 c 226 g 333 t
ORIGIN

Query Match 97.7%; Score 1090.4; DB 6; Length 1132;

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Best Local similarity 99.9%; Pred. No. 2.1e-206; Matches 1091; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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RESULT 7

HSA277247

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

1

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52

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240

Db

232

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291

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RESULT 8
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LOCUS Homo sapiens interleukin 22 (IL22) gene, complete cds.
DEFINITION AF387519
ACCESSION AF387519
VERSION AF387519.1 GI:14423570
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 8393)
AUTHORS Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
Yi,Q. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-2001) Molecular Biotechnology, University of
Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: SeattleSNPs. NHLBI Program for
Genomic Applications, UW-FHCRC, Seattle, WA (URL:
http://pga.mbt.washington.edu).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 133350)

Alzobrooks, S.L., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Benton, J., Bimago, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowles, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, E., Day-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisgied, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzger, M., Miller, A., Miner, G., Miner, Z., Moser, M., Neal, D., Nelson, D., Newton, J., Morgan, M., Morris, S., Moser, M., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogulu, M., Okwono, G., Oragunye, N., Owiedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Petrus, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoostari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Zhou, J., Wleczek, R., Wooden, S., Worley, K., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Zuchiatipati, R. and Gibbs, R.

Direct Submission

2 (bases 1 to 133350)

Worley, K.C.

Direct Submission

Submitted (05-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 133350)

Worley, K.C.

Direct Submission

Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2001 this sequence version replaced gi:12656660.

INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email [gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

#### ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

#### QUALSTAT-REPORT-----

----- Summary Statistics -----

Contig length: 150667

Phrap values in estimate: 149705

Average error rate (BCM-Phrap estimate): 1.52849e-05

Fraction of Phrap values less than 40 : 0.0163588

Number of consensus changing edits: 83

Number of N's in consensus : 0

----- Consensus changing edits -----

Position	Original	Context	Edited	Context
7824	tattatat(n)nnngtatact	tattatat(g)tggtatact	tattatat(g)tggtatact	tattatat(g)tggtatact
7825	attatat(n)nnngtatact	attatat(g)tggtatact	attatat(g)tggtatact	attatat(g)tggtatact
7826	ttatatnn(n)ngtatactat	ttatat(g)tggtatactat	ttatat(g)tggtatactat	ttatat(g)tggtatactat
7827	ttatatnn(n)ngtatactata	ttatat(g)tggtatactata	ttatat(g)tggtatactata	ttatat(g)tggtatactata
7855	atatatgc(n)acatttata	atatat(g)tggtatactata	atatat(g)tggtatactata	atatat(g)tggtatactata
8162	agaccacttt(n)tgagatggca	agaccact(g)tggtatactata	agaccact(g)tggtatactata	agaccact(g)tggtatactata
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19890	nnnnnnnnnn(n)nnnnnnnnng	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata
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19894	nnnnnnnnnn(n)nnnnnnnnng	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata
19895	nnnnnnnnnn(n)nnnnnnnnng	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata
19896	nnnnnnnnnn(n)nnnnnnnnng	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata	nnnnnnng(g)tggtatactata

19897	ctnaannnnn(n)ntnnnnnnnn	ctagatggcc(a)gttccattag	Db	1935	ATTGATAACATTTTCATTGTAACGGTCTCTATACACAGAAAAAATTTATTTTAAAT	1876
19898	tnaannnnn(n)tnnnnnnnnt	tagatggcca(g)ttccattagg	Qy	839	aatgtctttttccataaaagaattacttcttccattccttaggggaaaaaacccctaaa	898
19900	aannnnnnn(n)nnnnnnntn	gatggccatg(t)ccattaggag	Db	1875	AATTTGCTTTTCCATAAAAAGATTTACTTTCCATTCCTTTAGGGGAAAAAACCCCTAAA	1816
19901	nnnnnnnnn(n)nnnnntnn	tgccagttc(c)attaggagcag	Qy	899	tagttcatgtttccataatcagctactttatattataaatgtatttatttattattataa	958
19903	nnnnnnnnn(n)ennntnnng	ggccagttcc(a)ttaggagcag	Db	1815	TAGCTTCATGTTTCCATAAATCAGTACTTTATATTAATTAATGATTTATTTATTTATATAA	1756
19904	nnnnnnnnn(n)nnntnnngn	ggccagttcc(a)ttaggagcag	Qy	959	gactgcattttatttatcatctatttataataatgatttatttatagaacatcatcga	1018
19905	nnnnnnnnn(n)nnntnnngna	ggccagttcc(a)ttaggagcag	Db	1755	GACTGCATTTTATTTATATCATTTTATTAATTAATGATTTATTTATTTATTTATATAA	1696
19906	nnnnnnnnn(n)ntnnngnaa	agttccatt(a)ggcaggaagaa	Qy	1019	tattgtcactgtagtgtaaggcctaattatttatatttgacaatacttagagctataa	1078
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19910	nnnnnnnnn(t)nnngnaaanc	tcattattagg(c)aggaaacaag	RESULT 10			
19911	nnnnnnnnn(n)ngnaacanca	ccatattggcc(a)ggaaacaag	AC007458/c			
19914	nnnnnnnnn(n)gaacancac	ttagggcagg(a)aaacagcaga	LOCUS			
19919	tnngnaaaca(n)aacancacag	gaggaacaaca(a)gacaggtcag	DEFINITION			
19920	tnngnaaaca(n)caaggtcana	caggaacaaca(a)gacaggtcaga	AC007458			
19929	ncacaggtca(n)attttctgg	agacaggtca(g)attttctgg	AC007458.13			
19959	gtaattccag(n)aaanaccan	gttaattccag(t)aaanaccan	VERSION			
19963	naaanaccan(n)accaangtn	taaataccac(t)gttctctct	GI:5668755			
19969	naaanaccan(n)gttctctct	taaataccac(t)gttctctct	hmg.			
19973	naccacngtt(n)ctctctct	taccacngtt(t)ctctctct	human.			
43356	actatcatg(n)agtattgagt	actatcatg(a)agtattgagt	ORGANISM			
61290	aagacctgt(n)tcataaataa	aagacctgt(c)tcataaataa	Homo sapiens			
92985	tatatattct(n)aaatttaact	tatatattct(g)aaatttaact	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
93027	cagacatatg(a)gtgcacnctt	cagacatatg(t)gtgcacnctt	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
93034	atgagtgcac(n)cttgatnctc	atgagtgcac(g)cttgatnctc	1 (bases 1 to 191111)			
93041	catncttgat(n)tcctatttaa	catncttgat(g)tcctatttaa	Muzny, D., Arenson, A.D., Bouck, J., Bunac, C., Chen, Z., Ding, Y.,			
93047	tgatnctct(a)tcataaactat	tgatnctct(c)tcataaactat	Dugan, S., Durbin, J., Forcum, J., Garcia, C., Gorrell, J.H.,			
93107	atcatctca(n)tttctcttta	atcatctca(a)tttctcttta	Kordecki, N., Lau, S., Leal, B., Lee, E., Lichtarge, O., Liu, W.,			
105875	aagtccatg(n)caatgtcagg	aagtccatg(g)caatgtcagg	Kondejewski, N., Lau, S., Marondel, I., Martinez, C., Merscher, S., Miller, A.,			
124584	agtcacatg(n)ngtaggaact	agtcacatg(c)ngtaggaact	Logan, O., Lu, J., Osval, G., Pampell, L.R., Parish, B.J., Perez, L.,			
124585	ctggccaaca(n)gttgaaaccc	ctggccaaca(t)gttgaaaccc	Montgomery, K., Rives, C., Scherer, S.E., Shen, H., Shm, C., Simon, M.,			
125786	tcacagtaac(n)nnnaggctg	tcacagtaac(c)nnnaggctg	Rashid, N.D., Williams, A., Worley, K.C., Xhang, A.M., Yang, R., Yu, W.,			
125860	ccagactac(n)nnnaggctga	ccagactac(c)nnnaggctga	Vo, Q., Williamson, A., Worley, K.C., Xhang, A.M., Yang, R., Yu, W.,			
125861	ccagactacnn(n)nnnaggctga	ccagactac(c)nnnaggctga	Zhou, X., Kucherlapati, R., Nelson, D., Nickerson, E. and Gibbs, R.A.			
125862	agctacacnn(n)nnnaggctgag	agctacacnn(g)nnnaggctgag	Direct Submission			
125863	agctacacnn(n)nnnaggctgag	agctacacnn(g)nnnaggctgag	Unpublished			
125864	agctacacnn(n)nnnaggctgag	agctacacnn(g)nnnaggctgag	2 (bases 1 to 191111)			
126773	ttttcttttg(c)ttttctcttt	ttttcttttg(c)ttttctcttt	Worley, K.C.			
126811	agcagatc(c)ntctatnncc	agcagatc(c)ntctatnncc	Direct Submission			
126812	cgagactcn(n)tcataanncc	cgagactcn(c)tcataanncc	Submitted (04-MAY-1999)			
126818	tcnntctat(n)nnccngcttg	tcnntctat(c)nnccngcttg	College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
126820	cnctctatnn(n)cnngctgga	cnctctatnn(c)cnngctgga	Submitted (31-JUL-1999)			
126823	tcctatnncc(n)ggctggagtg	tcctatnncc(a)ggctggagtg	of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
Qy	479	aaagcttgagagagtgagagatcaaaagcaattggagaactggtattgctgtttatgct	REFERENCE			
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Qy	539	tctgagaaatcctgcatttaccagagcaagctgaaatgaataactaacccccctt	JOURNAL			
Db	2175	TCTGAAATGCTGCATTTGACAGAGCAAGCTGAAATGAATAACTAACCCCTTT	REFERENCE			
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Qy	779	attgataacatttcattgttaactggtgttctatcacagaaacatttttttaaat	AUTHORS			



JOURNAL

Submitted (25-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 31, 1999 this sequence version replaced gi:5230396.  
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email [gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.  
Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches, of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smil and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----  
Contig length: 151624  
Phrap values in estimate: 151315  
Average error rate (BCM-Phrap estimate): 0.000165522  
Fraction of Phrap values less than 40 : 5  
Number of consensus changing edits: 0  
Number of N's in consensus : 0

----- Consensus changing edits -----  
Position Original+Context Edited+Context  
2273 ggccttcatt(n)tcaattgttt ggccttcatt(t)tcaattgttt  
5088 agatgggtgc(n)tactctctcc agatgggtgc(c)tactctctcc  
102880 ggtttcactg(n)gttaactcagg ggtttcactg(t)gttaactcagg  
123710 tctataatt(n)tgtttataatg tctataatt(t)tgtttataatg  
127972 tttcttgag(n)gaatcctaag tttcttgag(t)gaatcctaag

----- Distribution of Quality < 40 Bases -----  
1000| \* \* \* \* \*  
900| \* \* \* \* \*  
800| \* \* \* \* \*  
700| \* \* \* \* \*  
# bases 600| \* \* \* \* \*  
500| \* \* \* \* \*  
400| \* \* \* \* \*  
300| \* \* \* \* \*  
200| \* \* \* \* \*

100| \* \* \* \* \*  
0| \* \* \* \* \*  
5 10 15 20 25 30 35 40  
phrap Value Range

FEATURES  
Source

Version: 1.01 qxfo.

Location/Qualifiers

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/function="Overlaps with adjacent clone AC005294"

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/complement(4043..7146)

/rpt\_family="LIPBb"

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/complement(8860..8988)

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/rpt\_family="LIMC/D"

/complement(9927..10097)

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10575..10852

/rpt\_family="AluJo"

11022..11060

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12877..12950

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14920..14949

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21218..21247

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21547..21661

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Matches 637; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 539 tctgagaatgctgcattgaccagagcaagctgaaaaatgaataactaaccccccttt 598
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Db 188185 TCTGAGAAATGCTGCTGATTGACAGAGCAAGCTGCAAAATGAATACTAACCCCTTT 188126

QY 599 cctctgataatacaaatagatcccaagcgatttttttaacaaaagaagaatg 658
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Db 188125 CCTGCTGAAATACAAATAGATGCCCAAGCAAGCAATTTTTTAAACCAAGGAAGATG 188066

QY 659 ggaagccaaactccatcatgagtggtgattcccaaatgaacccctgcgttagttacaag 718
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Db 188065 GGAAGCCAAATCCATCATGATGGTGGATTCCAAATGAACCCCTGCTTAGTTACAAG 188006

QY 719 gaaccaaactccactttgttataagaccagagagtgagactttctaagcatagatat 778
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Db 188005 GAAACCAATGCCACTTTTCTTTAAGACCAAGAGTAGACTTTCTAAGCATAGATATTT 187946

QY 779 attgataaacttcattgtaactggtggtctctacacagaaaacaattttttaaat 838
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Db 187945 ATTGATAACATTCATTGTAAGTGGTGTCTCTATACACAGAAACAATTTATTTTAAT 187886

QY 839 aattgtctttttccataaaagattactttccattcctcttaggggaaaaaacccctaaa 898
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Db 187885 AATTGTCTTTTCCATAAAAGATTACTTTTCCATTCTTCTAGGGGAAAAAACCCCTAAA 187826

QY 899 tagcttcattgcttaactgagcttatttataataatgatttattattattataa 958
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Db 187825 TAGCTTCATGTTTCCATAATACAGTACTTATATTTATAAATGATTTATTTATATATA 187766

QY 959 gactgattttattatcattttattattgatttatttattagaaacacatcttga 1018
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Db 187765 GACTGCAATTTTATTATCATTTTATTTATATGATGTTATTTTATAGAAACATCATTCGA 187706

QY 1019 tattgctacttgagtgagggcctaattgatattttattgacataattatagagctataa 1078
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Db 187705 TATTGCTACTTGAGTGAAGGCTAATTTGATATTTTATGACATAATTTATAGAGCTATA 187646

QY 1079 catgtttatttgacctcaataaacaacttgatataccta 1116
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Db 187645 CATGTTTATTGACCTCAATAAACACTTTGGATATCCTA 187608

RESULT 11
AC087562
LOCUS
DEFINITION
Pan troglodytes clone RP43-74117, WORKING DRAFT SEQUENCE, 31
unordered pieces.
AC087562
AC087562.4 GI:14190648
HTG: HTGS_PHASE1; HTGS_DRAFT.
chimpanzee.
Pan troglodytes
ORGANISM
Eukaryota; Metazoa; Chordata; Craniaria; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 135146)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-olsman,F.R., Allen,C.,
Alisbrooks,S.L., Anaratinge,H.C., Are,J.R., Banks,T., Barbajria,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonin,D., Bouck,J.,
Bowie,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

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\* 16497: gap of unknown length  
\* 16597: contig of 6039 bp in length  
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\* 39046: contig of 4862 bp in length  
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\* 4980: contig of 5834 bp in length  
\* 4981: gap of unknown length  
\* 4982: contig of 3606 bp in length  
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\* 4984: contig of 5933 bp in length  
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\* 5584: contig of 4765 bp in length  
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\* 5587: contig of 5560 bp in length  
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\* 5590: contig of 4748 bp in length  
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\* /db\_xref="taxon:9598"  
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ORIGIN

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Best Local Similarity 98.0%; Pred. No. 6.1e-102;

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Qy 574 gaaaaatgaataaatacccccttccctgctagataaatacaattagatgccccaaagcg 633  
Dy 28907 GAAAGATGAATAACTAACCCCTTTTCTGTGTAGAAATAACAATTAGATGCCCCAAGCG 28966  
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Dy 28967 ACTTTTTTTTACCCAAAAGGAAGATGGGAAGCAACATCCATCATGATTTGGTGGATTCCA 29026  
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Dy 29337 GATTTATTATTAGAAGCAATTCGATATTTGCTACTGAGTATAAGGCTAATATTGATAT 29386  
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Dy 29446 CCTA 29449  
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ARI65228  
LOCUS ARI65228 1111 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 9 from patent US 6274710.  
ACCESSION ARI65228  
VERSION ARI65228.1 GI:16238721  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1111)  
AUTHORS Dumoutier, L., Louhed, J., and Renauld, J.  
TITLE Antibodies which specifically bind T Cell inducible factors (TIFs)  
JOURNAL Patent: US 6274710-A 9 14-AUG-2001;  
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BASE COUNT 346 a 232 c 236 g 297 t  
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Query Match 47.1%; Score 525.2; DB 6; Length 1111;  
Best Local Similarity 73.8%; Pred. No. 2.7e-94;  
Matches 813; Conservative 0; Mismatches 253; Indels 36; Gaps 10;

Qy 15 tctgcaatggccgcctgcagaaatctgtgagctcttcttcttatgggaccctggccacc 74







GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:32:14 ; Search time 217.44 Seconds  
(without alignments)  
8811.978 Million cell updates/sec

Title: US-09-746-375-1

Perfect score: 1116

Sequence: 1 tcgagtagaattgtctgca.....ataaacacttggatattccta lll6

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*  
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18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	100.0	1116	22	Human cytokine, ZC
2	1116	100.0	1116	22	Human IL-TIF polyp
3	1116	100.0	1177	21	Human GIL-13/AE289
4	1114	99.8	1152	22	Human PRO10096 cDN
5	1114	99.8	1152	22	Nucleotide sequenc
6	1096.6	98.3	1139	22	Human interleukin-
7	1090.4	97.7	1132	22	Human EXCS encodin
8	639	57.3	690	21	Human T cell induc
9	639	57.3	690	22	Human cDNA encodin

10	526	47.1	1166	21	AAC81774	Murine GIL-19 prot
11	525.2	47.1	1111	21	AAA28817	Murine T cell indu
12	525.2	47.1	1111	22	AAA14860	Mouse cDNA for T c
13	524.4	47.0	1119	21	AAA28815	Murine T cell indu
14	524.4	47.0	1119	22	AAA14858	Mouse cDNA encodin
15	429.2	38.5	778	22	AAD09746	Mouse ZCYTO18 cDNA
16	380	34.1	537	22	AAF28842	Human interleukin-
17	356.4	31.9	501	22	AAD09720	Degenerate sequenc
18	270.4	24.2	504	21	AAA34354	Mouse secreted exp
19	216.4	19.4	5935	21	AAA28818	Murine T cell indu
20	216.4	19.4	5935	22	AAA14878	Mouse partial geno
21	215.6	19.3	7444	21	AAA28816	Murine T cell indu
22	215.6	19.3	7444	22	AAA14859	Mouse partial geno
23	207	18.5	4796	21	AAA28840	Human T cell induc
24	207	18.5	4797	22	AAA14876	Human partial geno
c 25	67.4	6.0	3296	23	ABL17264	Drosophila melanog
c 26	63.2	5.7	6243	20	AZ09598	Clostridium specie
c 27	62	5.6	6082	24	ABL33752	Human immune syste
c 28	61	5.5	113515	24	ABL34175	Human immune syste
29	60.4	5.4	14987	24	ABL32630	Human immune syste
30	60.2	5.4	7597	24	ABL33013	Human immune syste
c 31	59.8	5.4	19965	22	AAK73166	Human immune/haema
c 32	59.6	5.3	5413	22	AAK46694	Tumour suppressor
c 33	59.6	5.3	20420	22	AAK73165	Human immune/haema
34	58.4	5.3	5975	24	AAK61096	Human gene regulat
c 35	59.2	5.3	8786	23	ABL16590	Drosophila melanog
c 36	58.8	5.3	740	22	AAK42953	DNA encoding G pro
c 37	58.2	5.2	5487	24	ABL33598	Human immune syste
c 38	58.2	5.2	7456	24	ABL33931	Human immune syste
c 39	58	5.2	6641	24	ABL32315	Human immune syste
40	57.6	5.2	20420	22	AAK73165	Human immune/haema
41	57	5.1	6971	24	ABL33237	Human immune syste
c 42	56.8	5.1	19124	18	AAK72882	Plasmodium var-7 g
c 43	56.8	5.1	19124	21	AAZ98287	Plasmodium var-7 p
44	56.6	5.1	6175	24	ABL33307	Human immune syste
c 45	56.6	5.1	6298	22	AAK45359	Chemically pretrea

#### ALIGNMENTS

RESULT 1  
AAD09719 standard: cDNA: 1116 BP.  
ID AAD09719; AC AAD09719; DT 10-SEP-2001 (first entry) XX Human cytokine, ZCYTO18 cDNA.  
DE Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality; KW cancer; inflammation; gene therapy; chromosome 12; ss. OS Homo sapiens.  
XX Key Location/Qualifiers  
FH CDS 21..560  
FT /\*tag= a "Human ZCYTO18 protein #1"  
FT /\*product= a  
FT sig\_peptide 21..119  
FT /\*tag= b  
FT mat\_peptide 120..557  
FT /\*tag= c  
FT /\*product= "Human mature ZCYTO18 protein #1"  
FT CDS 57..560  
FT /\*tag= d  
FT sig\_peptide 57..119  
FT /\*product= "Human ZCYTO18 protein #2"  
FT mat\_peptide 120..557  
FT /\*tag= e  
FT /\*product= "Human mature ZCYTO18 protein #2"  
FT





XX (ZYMO ) ZYMOGENETICS INC.

PA Presnell SR, Xu W, Kindsvogel W, Chen Z;

PI WPI; 2001-356158/37.

DR P-PSDB; AAB62664.

XX New soluble cytokine receptor polypeptides and polynucleotides, useful  
PT for diagnosing and treating cancer and inflammatory conditions -

XX Example 17; Page 193-195; 210pp; English.

XX The invention relates to a human cytokine receptor polypeptide,  
CC designated zcytor16. The zcytor16 polypeptide can be expressed by  
CC standard recombinant methodology and can bind to IL-TIF (undefined). The  
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation  
CC or differentiation of hematopoietic cell(s) (progenitors); reducing  
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an  
CC inflammatory response in a mammal with inflammation. Heteromeric/  
CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be  
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides  
CC can also be used to detect IL-TIF levels which is indicative of  
CC pathological conditions including inflammatory states (e.g. rheumatoid  
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the  
CC polypeptides themselves are useful for the treatment of inflammation,  
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel  
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune  
CC diseases. The antibodies and zcytor16 polynucleotides are also useful  
CC for detecting cancer. The present sequence represents a cDNA encoding  
CC the human IL-TIF protein.

XX Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

Query Match 100.0%; Score 1116; DB 22; Length 1116;  
Best Local Similarity 100.0%; Pred. No. 2.9e-233; Indels 0; Gaps 0;  
Matches 1116; Conservative 0; Mismatches 0;

QY 1 tcgagttagaattgtctgaatggccgctcctgcagaaatctgtgagcttttccctattg 60  
DB 1 tcgagttagaattgtctgaatggccgctcctgcagaaatctgtgagcttttccctattg 60

QY 61 ggaacctggccaccagctgcctcctctctcttcttggccctctgtgtacaggaggagcagctg 120  
DB 61 ggaacctggccaccagctgcctcctctctcttcttggccctctgtgtacaggaggagcagctg 120

QY 121 cggccatcagctcccaactgcagcttgcaagctgcaactcccaactccagcagcctatacaca 180  
DB 121 cggccatcagctcccaactgcagcttgcaagctgcaactcccaactccagcagcctatacaca 180

QY 181 accgcaccttcctgctggttaaggaggtgagcttggctgatacaacacagacgcttcgtc 240  
DB 181 accgcaccttcctgctggttaaggaggtgagcttggctgatacaacacagacgcttcgtc 240

QY 241 tcaatggggagaaactgttccacgagtcagtatgagtgagcgtctatctgtatgaagc 300  
DB 241 tcaatggggagaaactgttccacgagtcagtatgagtgagcgtctatctgtatgaagc 300

QY 301 aggtgactgaactcacccttgaaagagtgctgttccctcaatctgataggttccagcctt 360  
DB 301 aggtgactgaactcacccttgaaagagtgctgttccctcaatctgataggttccagcctt 360

QY 361 atatgcaggaggtggtgacctccttggccaggtcagcaacaggttaacacatgtcata 420  
DB 361 atatgcaggaggtggtgacctccttggccaggtcagcaacaggttaacacatgtcata 420

QY 421 ttgaagggtgatgacctgcataccagaggaatgtgcacaaagctgaaggacacagtgaaaa 480  
DB 421 ttgaagggtgatgacctgcataccagaggaatgtgcacaaagctgaaggacacagtgaaaa 480

QY 481 agcttggagagagtgagagatcaagaacttggagagactgatttctgtttatgtctc 540  
DB 481 agcttggagagagtgagagatcaagaacttggagagactgatttctgtttatgtctc 540

Db 481 agcttggagagagtgagagatcaagaacttggagagactgatttctgtttatgtctc 540  
QY 541 tgagaaatgcctgcatttgaccagagcaagctgaaatgaataactaacccctttcc 600  
Db 541 tgagaaatgcctgcatttgaccagagcaagctgaaatgaataactaacccctttcc 600  
QY 601 ctgctagaaataacaattagatgccccaaagcgatttttttaacacaaaggaagatg 660  
Db 601 ctgctagaaataacaattagatgccccaaagcgatttttttaacacaaaggaagatg 660  
QY 661 aagccaaactccatcatgagtggtgattcccaatgaacccctggttagttacaaaga 720  
Db 661 aagccaaactccatcatgagtggtgattcccaatgaacccctggttagttacaaaga 720  
QY 721 aaccaatgccaactttgtttataagaccagaaggtagactttctaaagcatagatttat 780  
Db 721 aaccaatgccaactttgtttataagaccagaaggtagactttctaaagcatagatttat 780  
QY 781 tgataaacatttcattgtaactggttctctatcacagaaaaaacttttttttaataa 840  
Db 781 tgataaacatttcattgtaactggttctctatcacagaaaaaacttttttttaataa 840  
QY 841 ttgtctttttccataaaaaagattacttttccattctttaggggaaaaaacccctaaata 900  
Db 841 ttgtctttttccataaaaaagattacttttccattctttaggggaaaaaacccctaaata 900  
QY 901 gcttcattgtttccataaactcagctactttatttataaaatgtatttattattataaga 960  
Db 901 gcttcattgtttccataaactcagctactttatttataaaatgtatttattattataaga 960  
QY 961 ctgcattttatttataactttttattataatgagattttattatagaacacattcgata 1020  
Db 961 ctgcattttatttataactttttattataatgagattttattatagaacacattcgata 1020  
QY 1021 ttgctacttgagtgtaaggctaatatttgatttataacataattatagagctataaca 1080  
Db 1021 ttgctacttgagtgtaaggctaatatttgatttataacataattatagagctataaca 1080  
QY 1081 tgtttatttgacctcaataaacaacttggataccta 1116  
Db 1081 tgtttatttgacctcaataaacaacttggataccta 1116

RESULT 3

AAC81773

ID AAC81773 standard; cDNA; 1177 BP.

XX AC AAC81773;

XX DT 23-FEB-2001 (first entry)

XX Human GIL-19/AE289 protein coding sequence.

DE Human; GIL-19/AE289; IL-10; interleukin-10; nutrition;

KW cell proliferation; immune stimulation; immune suppression;

KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.

OS Homo sapiens.

XX PN WO200065027-A2.

XX PD 02-NOV-2000.

XX PF 28-APR-2000; 2000WO-US11479.

XX PR 28-APR-1999; 99US-0131473.

XX (GENY ) GENETICS INST INC.

XX PA Jacobs K, Fouser L, Spaulding V, Xuan D;

XX WPI; 2000-687325/67.

DR P-PSDB; AAB36292.

XX Human GIL-19 protein that shows a high degree of homology to IL  
PT (interleukin)-10, useful in upregulation of humoral immune responses,  
PT as an antiinflammatory agent and as a modulator of immune responses  
PT associated with injury -

XX Claim 1; Page 59; 60pp; English.

XX The present invention provides the protein and coding sequences for the  
CC novel human GIL-19/AE289 protein. The protein shows homology to  
CC interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used  
CC in the regulation of cell proliferation and differentiation,  
CC haematopoiesis, immune stimulation or suppression, tissue growth and  
CC tumour inhibition. In addition, it also has uses in the treatment of  
CC inflammation and in nutrition.

XX Sequence 1177 BP; 362 A; 245 C; 232 G; 338 T; 0 other;

Query Match 100.0%; Score 1116; DB 21; Length 1177;

Best Local Similarity 100.0%; Pred. No. 3e-233;

Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tcgagttagaattgtctgaatggccgcctgcagaaatctgtgagctcttctctatgg 60  
Db 45 tcgagttagaattgtctgaatggccgcctgcagaaatctgtgagctcttctctatgg 104  
Qy 61 ggaccctggccaccagctgctctctctctgtggccctctgtgtacaggagagcagctg 120  
Db 105 ggaccctggccaccagctgctctctctctgtggccctctgtgtacaggagagcagctg 164  
Qy 121 cgcccatcagctcccaatgcaggcttgacaagtcgaactccagcagccctatcacca 180  
Db 165 cgcccatcagctcccaatgcaggcttgacaagtcgaactccagcagccctatcacca 224  
Qy 181 accgcaacttcattgtctgaaggagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240  
Db 225 accgcaacttcattgtctgaaggagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 284  
Qy 241 tcattggggagaaactgtccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
Db 285 tcattggggagaaactgtccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 344  
Qy 301 aggtgtgaacttcaccccttgaagaagtcgtgttccctccatctgataggttccagcctt 360  
Db 345 aggtgtgaacttcaccccttgaagaagtcgtgttccctccatctgataggttccagcctt 404  
Qy 361 atatcaggaggtgtgtcccttccctggcagcagtcagcaacagcagtcagtcagtcagtc 420  
Db 405 atatcaggaggtgtgtcccttccctggcagcagtcagcaacagcagtcagtcagtcagtc 464  
Qy 421 ttgaaggtgatgacctgcataatccagaggaatgtgcaaaagctgaaggacagtcgaaaa 480  
Db 465 ttgaaggtgatgacctgcataatccagaggaatgtgcaaaagctgaaggacagtcgaaaa 524  
Qy 481 agcttggagagagtgagagatcaaaagcaattgggagaactgattgtgtttatgtctc 540  
Db 525 agcttggagagagtgagagatcaaaagcaattgggagaactgattgtgtttatgtctc 584  
Qy 541 tgagaaatgctctgcattttgacagagcaaaagctgaaaatgaaactaaacccctttcc 600  
Db 585 tgagaaatgctctgcattttgacagagcaaaagctgaaaatgaaactaaacccctttcc 644  
Qy 601 ctgctagaaataacaaatagatgccccaagcgatttttttaaccaaaggaagatggg 660  
Db 645 ctgctagaaataacaaatagatgccccaagcgatttttttaaccaaaggaagatggg 704  
Qy 661 aagccaaactccatcatgatgggtggattcccaaatgaacccctgcgttagttacaaga 720  
Db 705 aagccaaactccatcatgatgggtggattcccaaatgaacccctgcgttagttacaaga 764  
Qy 721 aaccaatgccactttgttttaaacacagagaggtagactttcttaagcatagatttat 780

Db 765 aaccaatgccactttgtttataagaccagaggtagacttttctaagcatagatttat 824  
Qy 781 tgataacatttcattgttaactggtgtctctatcacagaaaaaatttttttaataaa 840  
Db 825 tgataacatttcattgttaactggtgtctctatcacagaaaaaatttttttaataaa 884  
Qy 841 ttgtctttttccataaaaaagattactttccattcttccattctttaggggaaaaaacccctaaata 900  
Db 885 ttgtctttttccataaaaaagattactttccattcttccattctttaggggaaaaaacccctaaata 944  
Qy 901 gcttcattgtttccataaatacagacttattattataaatagtattattattattataaga 960  
Db 945 gcttcattgtttccataaatacagacttattattataaatagtattattattattataaga 1004  
Qy 961 ctgcattttatttatcatcttttataatgattgattttattatagaacacatcatcgata 1020  
Db 1005 ctgcattttatttatcatcttttataatgattgattttattatagaacacatcatcgata 1064  
Qy 1021 ttgtctacttgagtgtaaggctaataattgatattttatgcaataaattatagagctataa 1080  
Db 1065 ttgtctacttgagtgtaaggctaataattgatattttatgcaataaattatagagctataa 1124  
Qy 1081 tgtttatttgacctcaataaaacaccttggtatcccta 1116  
Db 1125 tgtttatttgacctcaataaaacaccttggtatcccta 1160  
RESULT 4  
AAF92134  
ID AAF92134 standard; CDNA; 1152 BP.  
XX AC AAF92134;  
XX DF 15-MAY-2001 (first entry)  
XX DE Human PRO10096 cDNA.  
XX KW Human; PRO protein; mapping: ss.  
XX OS Homo sapiens.  
XX PN WO200116318-A2.  
XX PD 08-MAR-2001.  
XX PF 24-AUG-2000; 2000WO-US23328.  
XX PR 01-SEP-1999; 99WO-US20111.  
XX PR 15-SEP-1999; 99WO-US21090.  
XX PR 07-DEC-1999; 99US-0169495.  
XX PR 09-DEC-1999; 99US-0170262.  
XX PR 11-JAN-2000; 2000US-0175481.  
XX PR 18-FEB-2000; 2000WO-US04341.  
XX PR 22-FEB-2000; 2000WO-US04414.  
XX PR 01-MAR-2000; 2000WO-US05601.  
XX PR 03-MAR-2000; 2000US-0187202.  
XX PR 25-APR-2000; 2000US-0199397.  
XX PR 22-MAY-2000; 2000WO-US14042.  
XX PR 05-JUN-2000; 2000US-0209832.  
XX PA (GETH ) GENENTECH INC.  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
XX WPI: 2001-183260/18.  
DR P-PSDB: AAB87602.  
XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
PT chromosome and gene mapping. -  
XX

PS Claim 2; Fig 153; 278pp; English.

XX The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

XX Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;

Query Match 99.8%; Score 1114; DB 22; Length 1152;  
Best Local Similarity 100.0%; Pred. No. 8.1e-233;  
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcgagttagaattgtctgcaatggcgcgcctgcagaaatctgtgagctttccctatgg 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 38 tcgagttagaattgtctgcaatggcgcgcctgcagaaatctgtgagctttccctatgg 97  
QY 61 gacccctggccaccagctgcctcctctcttctgcccctctgtgtacaggagagcagctg 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 98 ggaacctggccaccagctgcctcctctcttctgcccctctgtgtacaggagagcagctg 157  
QY 121 cgcctcatcagctcccaactcagcgttgacaagtcacaactccagcagccctatcacca 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 158 cgcctcatcagctcccaactcagcgttgacaagtcacaactccagcagccctatcacca 217  
QY 181 accgcacctctcatgctggcctgaaggagcttagcttggctgatacaacacagcgttcgtc 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 218 accgcacctctcatgctggcctgaaggagcttagcttggctgatacaacacagcgttcgtc 277  
QY 241 tcattggggagaaactgttccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 278 tcattggggagaaactgttccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 337  
QY 301 agtgctgaacttcaccccttgaaagtgctgttccctcaactctgataggttccagcctt 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 338 agtgctgaacttcaccccttgaaagtgctgttccctcaactctgataggttccagcctt 397  
QY 361 atatgcaggagtggtgcccctctcctgcccagctcagcaacagcgttaagcatgtcata 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 398 atatgcaggagtggtgcccctctcctgcccagctcagcaacagcgttaagcatgtcata 457  
QY 421 ttgaagggtgatgaactgcataccagagaaatgtgcaaaagctgaaggacacagtgaaaa 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 458 ttgaagggtgatgaactgcataccagagaaatgtgcaaaagctgaaggacacagtgaaaa 517  
QY 481 agcttgagagagtgagagatcaagcaatggagaactgattgtgtttatgtctc 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 518 agcttgagagagtgagagatcaagcaatggagaactgattgtgtttatgtctc 577  
QY 541 tgagaaatgcctgcatttgaccagagcaagctgaaaaatgaataactaaccccccttcc 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 578 tgagaaatgcctgcatttgaccagagcaagctgaaaaatgaataactaaccccccttcc 637  
QY 601 ctgctagaaataacaaatagatgcccacaaagcagattttttaaccaaagaagatggg 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 638 ctgctagaaataacaaatagatgcccacaaagcagattttttaaccaaagaagatggg 697  
QY 661 aagcacaactccatcatgatgggtggatcccaatgaacccctgcgttagttacaaaaga 720  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 698 aagcacaactccatcatgatgggtggatcccaatgaacccctgcgttagttacaaaaga 757  
QY 721 aaccaatgccactttgtttataagaccagaaggtagactttcttaagcatagatatattat 780  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 758 aaccaatgccactttgtttataagaccagaaggtagactttcttaagcatagatatattat 817  
QY 781 tgataacatttcatgttaactggttctctatcacagaaaaacatttttttaataaa 840  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 818 tgataacatttcatgttaactggtgtctctatcacagaaaaaatttttttaataaa 877  
QY 841 ttgtcttttccataaaaaagattactttccattctcttaggggaaaaaacccctaaata 900  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 878 ttgtcttttccataaaaaagattactttccattctcttaggggaaaaaacccctaaata 937  
QY 901 gttcctatgtttccataaatacagtcactttatattataaaatgtattattattataaga 960  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 938 gttcctatgtttccataaatacagtcactttatattataaaatgtattattattataaga 997  
QY 961 ctgcattttttattatcaatt 1020  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 998 ctgcattttttattatcaatt 1057  
QY 1021 ttgtctacttgagttaaggcctaattattgtattttatgacaataattatagagctataaca 1080  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 1058 ttgtctacttgagttaaggcctaattattgtattttatgacaataattatagagctataaca 1117  
QY 1081 tgtttatttgacctcaataaaacacttggatatcc 1114  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 1118 tgtttatttgacctcaataaaacacttggatatcc 1151

RESULT 5  
AAC87053  
ID AAC87053 standard; cDNA; 1152 BP.  
XX  
AC AAC87053;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of human polypeptide PRO10096.  
XX  
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;  
PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;  
PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;  
PRO1600; PRO9940; PRO9301; PRO187; PRO337; PRO1411; PRO4356;  
PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;  
PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;  
ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 58..597  
FT FT /\*tag= a  
FT sig\_peptide 58..156  
FT FT /\*tag= b  
XX  
PN WO200077037-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 22-MAY-2000; 2000WO-US14042.  
XX  
PR 15-JUN-1999; 99US-0139695.  
PR 20-JUL-1999; 99US-0145070.  
PR 26-JUL-1999; 99US-0145698.  
PR 17-AUG-1999; 99US-0149396.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US21547.  
PR 01-DEC-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28301.  
PR 07-DEC-1999; 99WO-US28565.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04342.  
PR 01-MAR-2000; 2000WO-US04414.  
PR 02-MAR-2000; 2000WO-US05601.  
PR

```

PR 20-MAR-2000; 2000MO-US07377.
PR 30-MAR-2000; 2000MO-US08439.
PR 15-MAY-2000; 2000MO-US13358.
PR 17-MAY-2000; 2000MO-US13705.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J;
PI Pooni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
XX WPI; 2001-050091/06.
DR P-PSDB; AAB31210.
DR
XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -
XX
XX Claim 2; Fig 63; 244pp; English.
XX
CC The present sequence encodes a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding of these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.
XX
XX Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;
50
Query Match 99.8%; Score 1114; DB 22; Length 1152;
Best Local Similarity 100.0%; Pred. No. 8.1e-233;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tcgagttagaattgtctgcaatggccgctgcagagaatctgtgagctcttccttatgg 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 ggacctggccaccagctgcctctctcttggccctcttggtagcaggaggagcagctg 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 98 ggacctggccaccagctgcctctctcttggccctcttggtagcaggaggagcagctg 157
QY 121 cgcctcagctcccaactgagcgttgcaagtcacaaacttccacagcagcctatcacca 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 158 cgcctcagctcccaactgagcgttgcaagtcacaaacttccacagcagcctatcacca 217
QY 181 accgacacctcagctgctgagcgttgagcgttgagcgttgagcgttgagcgttgctc 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 218 accgacacctcagctgctgagcgttgagcgttgagcgttgagcgttgagcgttgctc 277
QY 241 tcattggggagagaactgttccacgagtcagtatgagtgagcgtgctatctgtaggaagc 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 278 tcattggggagagaactgttccacgagtcagtatgagtgagcgtgctatctgtaggaagc 337
QY 301 aggtgctgaacttcaccttgagaagtgctgttccctcaatctgtaggttccagcctt 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 338 aggtgctgaacttcaccttgagaagtgctgttccctcaatctgtaggttccagcctt 397
QY 361 atatcagagagtggtgccccttcctggccagcgtcagcaacagcgttaacacatgtcata 420
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 398 atatcagagagtggtgccccttcctggccagcgtcagcaacagcgttaacacatgtcata 457

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QY 421 ttgaaggtgatgacctgcatactccagagggaattgtgcaaaagctgaaggacacacagtga 480
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 458 ttgaaggtgatgacctgcatactccagagggaattgtgcaaaagctgaaggacacacagtga 517
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 481 agcttgagagagtgagagatcaaaacaaattggagaaactggaattgtctgtttatgtctc 540
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 518 agcttgagagagtgagagagatcaaaacaaattggagaaactggaattgtctgtttatgtctc 577
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 541 tgagaataatcctgcatttgaccagagcaaaagctgaataactgaataactaaacccctttcc 600
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 578 tgagaataatcctgcatttgaccagagcaaaagctgaataactgaataactaaacccctttcc 637
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 601 ctgctgagaataacaataatagatgcccaaaagcgaatttttttaacaaaagaagaatggg 660
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 638 ctgctgagaataacaataatagatgcccaaaagcgaatttttttaacaaaagaagaatggg 697
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 661 aagcaaaactccatcagtggtggattccaaatgaacccctcgttagttacaaagga 720
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 698 aagcaaaactccatcagtggtggattccaaatgaacccctcgttagttacaaagga 757
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 721 aaccaatgccactttgtttataagaccagaggtagactttctaaagcatagatatttat 780
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 758 aaccaatgccactttgtttataagaccagaggtagactttctaaagcatagatatttat 817
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 781 tgataaactttcattgttaactgggtgtttctatcacagaaaaaacttttttttaataa 840
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 818 tgataaactttcattgttaactgggtgtttctatcacagaaaaaacttttttttaataa 877
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 ttgctctttccataaaaaagattactttccattctttaggggaaaaaacccctaaata 900
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 878 ttgctctttccataaaaaagattactttccattctttaggggaaaaaacccctaaata 937
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 901 gcttcattgtttccataaactcagtaactttatttataaagtatttatttattattataaga 960
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 938 gcttcattgtttccataaactcagtaactttatttataaagtatttatttattattataaga 997
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 961 ctgcaattttatttattatttatttatttatttatttatttatttatttatttatttattt 1020
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 998 ctgcaattttatttattatttatttatttatttatttatttatttatttatttatttattt 1057
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1021 ttgctcacttgatgtaaggctaaataattgataatttattgacaataattatagagctataaca 1080
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1058 ttgctcacttgatgtaaggctaaataattgataatttattgacaataattatagagctataaca 1117
QY 1081 tgtttatttgacctcaataaacaacttgatattcc 1114
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1118 tgtttatttgacctcaataaacaacttgatattcc 1151
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||
RESULT 6
AAF28841
ID AAF28841 standard; DNA; 1139 BP.
XX
XX AAF28841;
XX
XX 25-APR-2001 (first entry)
XX
XX Human interleukin-10 homologue IL-D110 DNA sequence.
XX
XX Anti-inflammatory; immunosuppressive; cytostatic; antirheumatic; human;
XX antiarthritic; dermatological; thyromimetic; gene therapy; inflammation;
XX interleukin 10 homologue; IL-D110; IL-D210; cytokine; tumour therapy;
XX haematopoietic cell; probe; immunogen; systemic lupus erythematosus;
XX rheumatoid arthritis; Hashimoto's autoimmune response; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 59..598
XX FT /*tag= a
XX FT /product= "IL-D110"
XX FT /transl_except= (pos:245..247,aa:Xaa)

```

FT sig\_peptide /note= "Xaa-unknown"  
 FT 59..157 /\*tag= b  
 FT mat\_peptide 158..595 /\*tag= c  
 XX  
 PN WO200073457-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 26-MAY-2000; 2000WO-US14729.  
 PF  
 XX 27-MAY-1999; 99US-0322806.  
 PR  
 XX (SCHE ) SCHERING CORP.  
 PA  
 XX Parham CL, De Waal Malefyt R, Marehalli NL;  
 PI  
 XX WPI; 2001-061539/07.  
 DR P-PSDB; AAB37122.  
 XX

New interleukin-D110 genes and polypeptides useful for treating conditions associated with abnormal physiology, particularly e.g. inflammatory or autoimmune disorders

Claim 3; Page 51-52; 62pp; English.

This sequence represents the gene sequence for a human interleukin 10 homologue IL-D110. The invention also relates to another IL-10 homologue ID-210 (AAF28842). The IL-D110 is useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions, either acute or chronic. The new cytokine also plays a role in the regulation or development of haematopoietic cells, e.g. lymphoid or myeloid cells, which affect immunological responses, such as inflammation and/or autoimmune disorders. These may also be used in drug screening to identify compounds having binding affinity to or other relevant biological effects on IL-D110 functions, in anti-tumour therapy, as probes for detecting IL-D110 levels in samples from patients suspected of having an abnormal condition, e.g. autoimmune or inflammatory, in raising or screen antibodies, as immunogen, in diagnostic assays, and in detecting, isolating or identifying a DNA clone encoding IL-D110 or IL-D210 from a natural source. IL-D110 antagonists may be used to block immune responses, e.g. in situations as inflammatory or autoimmune responses, including rheumatoid arthritis, systemic lupus erythematosus, or Hashimoto's autoimmune responses.

Sequence 1139 BP; 337 A; 238 C; 227 G; 333 T; 4 other;

Query Match 98.3%; Score 1096.6; DB 22; Length 1139;  
 Best Local Similarity 99.5%; Pred. NO. 4.9e-229;  
 Matches 1096; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 tcgagttagaattgtctgaatggccgacctgacagaaatctgtgaccttttccttagg 60  
 DB |||||||  
 QY 61 ggacctggccaccagctgacctctctcttggccctcttggtacaggagagcagctg 120  
 DB |||||||  
 QY 99 ggacctggccaccagctgacctctctcttggccctcttggtacaggagagcagctg 158  
 DB |||||||  
 QY 121 cggccatcagctcccaactgagcgttgacaagtcacaactccagcagccctatacaca 180  
 DB |||||||  
 QY 159 cggccatcagctcccaactgagcgttgacaagtcacaactccagcagccctatacaca 218  
 DB |||||||  
 QY 181 accgcacctctcgtgctgaaggagcgtgacctggtgatacaacacagacgctgctc 240  
 DB |||||||  
 QY 219 accgcacctctcgtgctgaaggagcgtgacctggtgatacaacacagacgctgctc 278  
 DB |||||||  
 QY 241 tcaattggggagaaactgttccacgagtcagtcagtgtgagcgctgctatctgtagaacg 300  
 DB |||||||  
 QY 279 tcaattggggagaaactgttccacgagtcagtcagtgtgagcgctgctatctgtagaacg 338  
 DB |||||||

QY 301 aggtgtgaacttcaccttggaagtgctgttccctcaatctgataggttccagcctt 360  
 DB |||||||  
 QY 339 aggtgtgaacttcaccttggaagtgctgttccctcaatctgataggttccagcctt 398  
 DB |||||||  
 QY 361 atatcaggagtggtgccccttcctggccagctcagcaaacaggcttaagcaatgtcata 420  
 DB |||||||  
 QY 399 atatcaggagtggtgccccttcctggccagctcagcaaacaggcttaagcaatgtcata 458  
 DB |||||||  
 QY 421 ttgaaggtgatgacctgcacatccacagaggaatgtgcaaaagctgaagggacacagtgaaaa 480  
 DB |||||||  
 QY 459 ttgaaggtgatgacctgcacatccacagaggaatgtgcaaaagctgaagggacacagtgaaaa 518  
 DB |||||||  
 QY 481 agcttgagagagtgagagatcaaaagcaattgggagacgtgatttgcgtgttatgtctc 540  
 DB |||||||  
 QY 519 agcttgagagagtgagagatcaaaagcaattgggagacgtgatttgcgtgttatgtctc 578  
 DB |||||||  
 QY 541 tgagaaatgctgcatttgaccagagcaaaagctgaaaaatgaataactaacccccctttcc 600  
 DB |||||||  
 QY 579 tgagaaatgctgcatttgaccagagcaaaagctgaaaaatgaataactaacccccctttcc 638  
 DB |||||||  
 QY 601 ctgctagaaataacaaatagatgcccccaaacgatttttttaacccaaaggaagatggg 660  
 DB |||||||  
 QY 639 ctgctagaaataacaaatagatgcccccaaacgatttttttaacccaaaggaagatggg 698  
 DB |||||||  
 QY 661 aagccaaactccatcatgatgggtgattcccaaatgaaacctgcgtgtgtacaaagga 720  
 DB |||||||  
 QY 699 aagccaaactccatcatgatgggtgattcccaaatgaaacctgcgtgtgtacaaagga 758  
 DB |||||||  
 QY 721 aaccaatgccaattttgtttataagaccagagaggttagacctttcctaagcagatatttat 780  
 DB |||||||  
 QY 759 aaccaatgccaattttgtttataagaccagagaggttagacctttcctwagcagatatttat 818  
 DB |||||||  
 QY 781 tgatacaatttcattgtaactggtgtctctacacagaaaaacaatttttttaataaa 840  
 DB |||||||  
 QY 819 tgatacaatttcattgtaactggtgtctctacacagaaaaacaatttttttaataaa 878  
 DB |||||||  
 QY 841 ttgttttttccataaaaaagattactttccattcctttagggggaaaaaacccctaaata 900  
 DB |||||||  
 QY 879 ttgttttttccataaaaaagattactttccattcctttagggggaaaaaacccctaaata 938  
 DB |||||||  
 QY 901 gcttcattgttccataaacagtcactttattataaaatgattattattattattataaga 960  
 DB |||||||  
 QY 939 gcttcattgttccataaacagtcactttattataaaatgattattattattattataaga 998  
 DB |||||||  
 QY 961 ctgcattttatttatcatctttattataatgattattattattataagaacatttcgata 1020  
 DB |||||||  
 QY 999 ctgcattttatttatcatctttattataatgattattattattataagaacatttcgata 1058  
 DB |||||||  
 QY 1021 ttgtctacttgagtgtaaggcctaattatgattattatgacaataattatagagctataaca 1080  
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 QY 1059 ttgtctacttgagtgtaaggcctaattatgattattatgacaataattatagagctataaca 1118  
 DB |||||||  
 QY 1081 tgtttatttgacctcaataaa 1101  
 DB |||||||  
 QY 1119 tgtttatttgacctcaatgaa 1139  
 DB |||||||

RESULT 7

AAC84310

ID AAC84310 standard; cDNA; 1132 BP.

XX AAC84310;

XX AC AAC84310;

XX DT 19-MAR-2001 (first entry)

XX DE Human EXCS encoding cDNA (clone ID 5571181CB1).

XX KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;

XX KW immunosuppressive; cytosolic; neuroprotective; gastroenteric;

XX KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;

XX KW antifertility; cerebroprotective; nootropic; antitumor; antifungal;

XX KW anticonvulsant; tranquilizer; neuroleptic; vasodilator; gynecological;

XX KW keratolytic; protozoacide; gene therapy; ss.



ID AAA28839 standard; cDNA; 690 BP.  
 AC AAA28839;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX  
 DE Human T cell inducible factor cDNA.  
 XX  
 KW TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;  
 KW Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;  
 KW probe; chromosome 12q15; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 72..611  
 FT /\*tag= a  
 FT  
 XX  
 XX WO200024758-A1.  
 XX  
 PD 04-MAY-2000.  
 XX  
 PF 18-OCT-1999; 99WO-US24424.  
 XX  
 XX 26-OCT-1998; 98US-0178973.  
 PR 16-JUL-1999; 99US-0354243.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 XX Dumoutier L, Louhed J, Renaud J;  
 XX  
 XX WPI; 2000-422495/36.  
 DR P-PSDB; AAY92879.  
 XX  
 XX New nucleic acid molecule encoding a T cell derived inducible factor  
 PT for treating asthma, an allergy or lymphoma  
 XX  
 PS Claim 1; Page 38; 46pp; English.  
 XX  
 CC This cDNA encodes a human T cell derived inducible factor (TIF). The gene  
 CC was mapped to chromosome 12q15. The human TIF was identified based on  
 CC homology to a murine TIF, which was identified by subtraction cloning  
 CC from a murine lymphoma cell line BW5147 in the presence or absence of  
 CC interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to  
 CC add any cytokines to its culture medium. Many IL-9 activities are  
 CC mediated by activation of STAT transcription factors. The novel TIFs were  
 CC expressed in the presence of IL-9, but not in its absence. TIFs induce  
 CC STAT activation in cells. They can be used, e.g. in the stimulation of  
 CC regeneration of targeted tissues. Their inhibitors or antagonists can be  
 CC used to retard, prevent or inhibit differentiation of other tissues. The  
 CC TIFs and their coding sequences are useful in the treatment of asthma,  
 CC allergies and lymphoma (claimed). They are also useful for identifying  
 CC compounds that inhibit or activate T cell induced factor activity in a  
 CC cell (claimed).  
 XX  
 SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;  
 Query Match 57.3%; Score 639; DB 21; Length 690;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-129;  
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 52 tcgagtagaattgtctgcaatggcgccctgacagaatctgtgagctcttccctatgg 111  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 ggacctggccaccagctcctcctctctcttggccctctgtacaggaggagcagctg 120  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 112 ggacctggccaccagctcctcctctcttggccctctgtacaggaggagcagctg 171  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 cggccatcagctcccaactcagcttgacaagtcacaactccagagccctatatcacca 180  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 172 cggccatcagctcccaactcagcttgacaagtcacaactccagagccctatatcacca 231  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 accgcaccttcattgctggctaaaggagctagcttggtctgataacaacacagacgttcgtc 240  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 232 accgcaccttcattgctggctaaaggagctagcttggtctgataacaacacagacgttcgtc 291  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 tcattggggagaaaaactgttccacggagtcagtatgtagtgagcgtctctatctgatgaagc 300  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 292 tcattggggagaaaaactgttccacggagtcagtatgtagtgagcgtctctatctgatgaagc 351  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 aggtgctgaactccaccttgaagaagtcgtgtccctcaatctgtaggttccagcctt 360  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 352 aggtgctgaactccaccttgaagaagtcgtgtccctcaatctgtaggttccagcctt 411  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 361 atatgcagagaggtggtgccccttctgcccaggtcagcaacaggtcgaagcacatgtcata 420  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 412 atatgcagagaggtggtgccccttctgcccaggtcgaagcacatgtcata 471  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 421 ttgaagtgatgacctgcataatccacagaggaatgtgcacaagctgaaggacacagtgaaaa 480  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 472 ttgaagtgatgacctgcataatccacagaggaatgtgcacaagctgaaggacacagtgaaaa 531  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 481 agcttgagagagtgagagatcaaaagcaattggagaaactggagaaactgttctgtttatgtctc 540  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 532 agcttgagagagtgagagatcaaaagcaattggagaaactgttctgtttatgtctc 591  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 541 tgagaaatgcctgcatttgaccagagcaaaagctgaaaaatgaaataactaaccccccttcc 600  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 592 tgagaaatgcctgcatttgaccagagcaaaagctgaaaaatgaaataactaaccccccttcc 651  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 601 ctgctagaataacaattagatgcccccaagcgattttt 639  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 652 ctgctagaataacaattagatgcccccaagcgattttt 690  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 9  
 AAS14875  
 ID AAS14875 standard; cDNA; 690 BP.  
 XX  
 AC AAS14875;  
 XX  
 DT 19-DEC-2001 (first entry)  
 XX  
 DE Human cDNA encoding T cell derived inducible factor, TIF.  
 XX  
 KW Human; T cell derived inducible factor; TIF; ss; antiallergic;  
 KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;  
 KW cancer; lymphoma; immune system disorder; allergy; asthma;  
 KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;  
 KW thyroiditis; melanoma; hepatoma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 72..611  
 FT /\*tag= a  
 FT /product= "TIF"  
 FT /transl\_except= (pos:159..161,aa:Glu)  
 FT /transl\_except= (pos:378..380,aa:Ile)  
 FT /transl\_except= (pos:405..407,aa:Arg)  
 FT /transl\_except= (pos:519..521,aa:Cys)  
 XX  
 XX US2001024652-A1.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 29-DEC-2000; 2000US-0751797.  
 XX  
 XX 18-OCT-1999; 99US-0419568.  
 PR 26-OCT-1998; 98US-0178973.  
 PR 16-JUL-1999; 99US-0354243.  
 XX  
 XX (DUMO/) DUMOUTIER L.  
 PA (LOUA/) LOUAHED J.

PA (RENAUD) RENAULD J.  
XX Dumoutier L, Louahed J, Renaud J;  
XX  
XX  
XX WPI: 2001-638496/73.  
DR P-PSDB; AAU09091.  
XX  
XX New isolated nucleic acid molecules encoding T cell inducible factors,  
PT useful as markers for expression or effect of interleukin (IL)-9 in a  
PT subject and diagnosing susceptibility to asthma or allergy  
XX  
XX Claim 1; Page 17; 26pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule, which encodes  
CC a T cell derived inducible factor (TIF) which are upregulated by the  
CC cytokine interleukin-9 (IL-9) and induce SPAT transcription factor  
CC activation. The TIF proteins (or their mutants) may be used to test IL-9  
CC ant/agonists for their potency against lymphomas, immune system  
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),  
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration  
CC or inhibit differentiation of tissue types in which they are active and  
CC therefore be used to develop treatments for melanomas and hepatomas.  
CC The present sequence encodes human TIF.  
XX  
XX Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;  
SQ

Query Match 57.3%; Score 639; DB 22; Length 690;  
Best Local Similarity 100.0%; Pred. No. 1.3e-129;  
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tcgagttagaattgtctgcaatggcgcctgcagaaatctgtgagctctttccctatgg 60  
Db |||||||  
Oy 52 tcgagttagaattgtctgcaatggcgcctgcagaaatctgtgagctctttccctatgg 111  
Db |||||||  
Oy 61 ggaacctggccaccagctgctctctctctctctctctctctctctctctctctctct 120  
Db |||||||  
Oy 112 ggaacctggccaccagctgctctctctctctctctctctctctctctctctctctct 171  
Db |||||||  
Oy 121 ggaacctggccaccagctgctctctctctctctctctctctctctctctctctctct 180  
Db |||||||  
Oy 172 ggaacctggccaccagctgctctctctctctctctctctctctctctctctctctct 231  
Db |||||||  
Oy 181 accgacaccttcattgctgctgctgctgctgctgctgctgctgctgctgctgctgct 240  
Db |||||||  
Oy 232 accgacaccttcattgctgctgctgctgctgctgctgctgctgctgctgctgctgct 291  
Db |||||||  
Oy 241 tcattggggagagaactgttccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
Db |||||||  
Oy 292 tcattggggagagaactgttccacgagtcagtcagtcagtcagtcagtcagtcagtcagtc 351  
Db |||||||  
Oy 301 aggtgtgaacttcacaccttgaaagagtcgtgttccctcaactctgattggttccagcctt 360  
Db |||||||  
Oy 352 aggtgtgaacttcacaccttgaaagagtcgtgttccctcaactctgattggttccagcctt 411  
Db |||||||  
Oy 361 atatgcaggaggtggtgcttcccttcctgcccaggtcagcaacaggctgaagcattgtcata 420  
Db |||||||  
Oy 412 atatgcaggaggtggtgcttcccttcctgcccaggtcagcaacaggctgaagcattgtcata 471  
Db |||||||  
Oy 421 ttgaagggtgattgacctgcatatccagaggaattgtcacaagctgaaggacagtgaaa 480  
Db |||||||  
Oy 472 ttgaagggtgattgacctgcatatccagaggaattgtcacaagctgaaggacagtgaaa 531  
Db |||||||  
Oy 481 agcttggagagagtgagagatcaaaagcaattggagaactgatttgcgtttatgtcttc 540  
Db |||||||  
Oy 532 agcttggagagagtgagagatcaaaagcaattggagaactgatttgcgtttatgtcttc 591  
Db |||||||  
Oy 541 tgagaaatgcctgcattttgaccagagcaaatgctgaaatgaaatgaaatgaaatgaaatgaaat 600  
Db |||||||  
Oy 592 tgagaaatgcctgcattttgaccagagcaaatgctgaaatgaaatgaaatgaaatgaaatgaaat 651  
Db |||||||  
Oy 601 ctgctagaataaataattagatgcccaaacgattttt 639  
Db |||||||

Db 652 ctgctagaataaataattagatgcccaaacgattttt 690

RESULT 10  
AAC81774  
ID AAC81774 standard; cDNA; 1166 BP.  
XX  
XX AAC81774;  
XX AC  
XX 23-FEB-2001 (first entry)  
XX DT  
XX Murine GIL-19 protein coding sequence.  
XX DE  
XX Mouse; GIL-19/AE289; IL-10; Interleukin-10; nutrition;  
XX KW cell proliferation; immune stimulation; immune suppression;  
XX KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.  
XX OS Mus sp.  
XX PN WO200065027-A2.  
XX PD 02-NOV-2000.  
XX PF 28-APR-2000; 2000WO-US11479.  
XX PR 28-APR-1999; 99US-0131473.  
XX PA (GEMY) GENETICS INST INC.  
XX PI Jacobs K, Fouser L, Spaulding V, Xuan D;  
XX WPI: 2000-687325/67.  
XX Human GIL-19 protein that shows a high degree of homology to IL  
XX (interleukin)-10, useful in upregulation of humoral immune responses,  
XX as an antiinflammatory agent and as a modulator of immune responses  
XX associated with injury -  
XX PS Disclosure: Fig 1; 60pp; English.  
XX The present invention provides the protein and coding sequences for the  
XX novel human GIL-19/AE289 protein. The protein shows homology to  
XX interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used  
XX in the regulation of cell proliferation and differentiation,  
XX haematopoiesis, immune stimulation or suppression, tissue growth and  
XX tumour inhibition. In addition, it also has uses in the treatment of  
XX inflammation and in nutrition.  
XX SQ Sequence 1166 BP; 375 A; 241 C; 244 G; 306 T; 0 other;

Query Match 47.1%; Score 526; DB 21; Length 1166;  
Best Local Similarity 74.4%; Pred. No. 5.7e-105;  
Matches 820; Conservative 0; Mismatches 245; Indels 37; Gaps 11;

Oy 15 tctgcaatggcgcgcctgcagaaatctgtgagcttcttcttcttcttcttcttcttcttcttct 74  
Db |||||||  
Oy 69 tctctgagtggtctgctgcagaaatctgtgagcttcttcttcttcttcttcttcttcttcttct 128  
Db |||||||  
Oy 75 agctgcctctctcttggcctctctgtcacaggaggagcagctgcgccatcagctcc 134  
Db |||||||  
Oy 129 agctgcctgcttctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 188  
Db |||||||  
Oy 135 caactcagagcttgcagaagtcacacttccagcagcgccttatatcaccaacccgaccttcctg 194  
Db |||||||  
Oy 189 cgggtcgaagcttgagggtgtcccaacttccagcagcgccttatatcaccaacccgaccttcctg 248  
Db |||||||  
Oy 195 ctggcttaagagagctgagcttgctgataacaacagagcttcttcttcttcttcttcttcttct 254  
Db |||||||  
Oy 249 ctggcgaagagggcagccttgcagataacaacagagcttcttcttcttcttcttcttcttct 308  
Db |||||||  
Oy 255 ctggtccacggagctgagtgagtgagctgcttcttcttcttcttcttcttcttcttcttcttct 314  
Db |||||||



Db 309 ctgttcgagagtgatgctgaagatgaagtgctacatgataagcagaggtgctcaattc 368  
 Qy 315 accctgaagaagtgctgttccctcaactctgataggttccagccttatatcagaggtg 374  
 Db 369 accctggaagagctgtgtctcccccagtcagacaggttccagcctcatatcagaggtg 428  
 Qy 375 gtgcccctctctggcagcgtcgaacacagcgtgaagcagatgtctatattgaaggtgatgac 434  
 Db 429 gtgcccctctctgacccaactcagaatcagctcagctcagctcagctcagcagcgtgacgac 488  
 Qy 435 ctgcatatcagaggaatgtgcgaacagctgaagacacagtgaaaaagccttggaagagt 494  
 Db 489 cagaacatcccagaagaatgtcagaagcgtcgaagagacagtgaaaaagccttggaagagt 548  
 Qy 495 ggaagatcaaaagcaattggagaactggattgtgtgtttatgtctctgagaaatgctctgc 554  
 Db 549 ggaagatcaagcgattgggaactggacctgtgtttatgtctctgagaaatgctctgc 608  
 Qy 555 attgacacagcaagcgtgaacaaatgaataactaaacccccttccctgctgagaaataac 614  
 Db 609 gtctgagcgaagaagctgaaacacgaagaactgctcctctcctgcttcttaaaaaaac 668  
 Qy 615 aatcagatcccccaagcgtatttttttaaccacaaagagatgggaagcacaactccat 674  
 Db 669 aataagatccccgaatggactttttta-----ctaaggaagtgagaagctaacgtccat 724  
 Qy 675 catgatgggtggtattcccaaatgaacccctgcgttagttacaaaggaacccaatgccactt 734  
 Db 725 cattattagaagatttcacatgaacactggctcagttgaaaaagaaaaatagtgcaa--g 782  
 Qy 735 ttgtttataagacagaggttagactttcttaagcatagatatttatgataacatttcat 794  
 Db 783 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaaattttat 841  
 Qy 795 tgaactgggtttctatacagacagaaacaaattttttttaaataattgtctttttccat 854  
 Db 842 tgcactgatg----atacacagaaataaatagtacttttaaaaaatgtctt-----g 890  
 Qy 855 aaaaaagattacttccattctcttaggggaacaaacccctaaatagcttctcatgtttcca 914  
 Db 891 aaaggaggttaccctcattccttta---gaaaaaagcttatgtaacttca--tttcca 945  
 Qy 915 taatcagactttattattataaagatgtattattattattattataagacgtgcaatttatta 974  
 Db 946 taaccaataattttattatgttaagtattattattattataagata-----cattttatta 999  
 Qy 975 tatcattttataatggattttattatagaacacatcttcgatattgtactacttgagt 1034  
 Db 1000 tgtcagtttataataatggattttattattataagaaacattatcgtctgtatgata-tttagta 1058  
 Qy 1035 taaggcctaatttgatatattatgacaataattatagagctataacatgtttattttgacct 1094  
 Db 1059 taaggcaata--atattatgacaataactatgg---aaacaagataatcttaggctt 1111  
 Qy 1095 caataaacacttgatatccta 1116  
 Db 1112 taataaacacatggatatcata 1133

## RESULT 11

AAA28817  
 ID AAA28817 standard; cDNA; 1111 BP.

XX  
 AC  
 AC  
 AA28817;

DT 04-SEP-2000 (first entry)

XX Murine T cell inducible factor beta cDNA.

DE TIF-beta; T cell derived inducible factor; interleukin 9; STAT; IL-9;  
 KW Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.

XX  
 OS Mus sp.

XX FH Key Location/Qualifiers  
 FT CDS 50..589  
 XX /\*tag= a  
 PN MO200024758-A1.  
 XX PD 04-MAY-2000.  
 XX PF 18-OCT-1999; 99WO-US24424.  
 XX PR 26-OCT-1998; 98US-0178973.  
 PR 16-JUL-1999; 99US-0354243.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Dumoutier L, Louhed J, Renauld J;  
 DR WPI; 2000-422495/36.  
 DR P-PSDB; AAY92878.  
 XX PT New nucleic acid molecule encoding a T cell derived inducible factor  
 PT for treating asthma, an allergy or lymphoma  
 XX PS Claim 1; Page 33-34; 46pp; English.  
 CC This cDNA encodes T cell derived inducible factor (TIF) beta identified  
 CC by subtraction cloning of a murine lymphoma cell line BW5147 in the  
 CC presence or absence of interleukin 9 (IL-9). There was a great deal of  
 CC homology with TIF-alpha cDNA (AA28815). The main difference was that  
 CC the promoters where not homologous suggesting independent regulation.  
 CC BW5147, can be grown in vitro, without the need to add any cytokines to  
 CC its culture medium. Many IL-9 activities are mediated by activation of  
 CC STAT transcription factors. The novel TIFs were expressed in the presence  
 CC of IL-9, but not in its absence. TIFs induce STAT activation in cells.  
 CC They can be used, e.g. in the stimulation of regeneration of targeted  
 CC tissues. Their inhibitors or antagonists can be used to retard, prevent  
 CC or inhibit differentiation of other tissues. The TIFs and their coding  
 CC sequences are useful in the treatment of asthma, allergies and lymphoma  
 CC (claimed). They are also useful for identifying compounds that inhibit or  
 CC activate T cell induced factor activity in a cell (claimed).  
 XX SQ Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;

Query Match 47.1%; Score 525.2; DB 21; Length 1111;  
 Best Local Similarity 73.8%; Pred. No. 8.3e-105;  
 Matches 813; Conservative 0; Mismatches 253; Indels 36; Gaps 10;

Qy 15 tctgcaatggccgcctcgacgaataatctgtgagctcttctcttatgggacccctggccacc 74  
 Db 44 tcggtgatggctgctcccgacgaatactatgatgttttcccttatgggacatttggccgc 103  
 Qy 75 agctgcctcctctctctgtggccctcttggtagagggagagcagctgogcccatcagctcc 134  
 Db 104 agctgcctgcttctcattgcctgtggcccgagggcgaatggctgcccatacaacc 163  
 Qy 135 cactcagagcttgacaagctccaactccagacccctatatatcaccacccgacacttcag 194  
 Db 164 cggctgaagcttgagggtgtccaaactccagcgcgtacatcgtaaccgacactttatg 223  
 Qy 195 ctggctaaaggaggttagcttggtgataaacaacagacagcttcctcatggggagagaa 254  
 Db 224 ctggccaaaggagggcagccttgacagataaacaacagacgctccggtcatcggggagaa 283  
 Qy 255 ctgttccacgagtgatgatgatgagcgtgtctatctgtatgaagcaggtgtcgaactc 314  
 Db 284 ctgttccgagagtgatgctgaagtcagtgctacactgatgaagcaggtgtcgaactc 343  
 Qy 315 acccttgaagaagtgctgttccctcaactctgataggtttccagccttatatcagaggtg 374  
 Db 344 accctggaagacattctgctccccagtcagacaggttccccgacctacatcagaggtg 403





Db 646 aataagatccctgaatggaactttttta-----ctaaggaaagtgaagaactaacgtccat 701  
Qy 675 catgagtggtggtatcccaatgaaccctcggttagttacaaggaaacaaatgcacatt 734  
Db 702 catcattagaagattccatgaacccctggtcagttgaaaggaaatagtgtcaa--g 759  
Qy 735 ttgtttataagaccagagagtagactttctaagcatagatatattattgataaacatttcat 794  
Db 760 ttgtccatgagaccag--agtagacttgataaccacaaagattccatgacaatttttat 818  
Qy 795 tgaactggtgttctctacacagaaacaaatatttttttaataatattgtctttttccat 854  
Db 819 tgtcactgatg---atacacagaaataatgtacttttaaaaaattgttt-----g 867  
Qy 855 aaaaaagattacttccattccctcttaggggaaaaaacccctaaatagcttcatgtttcca 914  
Db 868 aaaggaggttacctctctattcccttta---gaaaaaaagcttatgtaacttca--tttcca 922  
Qy 915 taatcagtagctttattataatgattattattattattattattataagactgtttatttg 974  
Db 923 tatccaatattttatatatgtaagttattattattattataagata-----cattttattta 976  
Qy 975 tatcattttattataatgattattattattataagaaacatcattcgattattgctacttgagt 1034  
Db 977 tgtcagtttattataatgattattattattataagaaacattatctgctattgata--tttagta 1035  
Qy 1035 taagcttaattattgattattatgacaataatattatagagctataacatgtttatttgacct 1094  
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Qy 1095 caataaacacttggatattccta 1116  
Db 1089 taataaacacatggatattcata 1110

RESULT 14  
AAS14858  
ID AAS14858 standard; cdna; 1119 BP.  
AC AAS14858;  
XX  
XX 19-DEC-2001 (first entry)  
DE Mouse cDNA encoding T cell derived inducible factor, TIFalpha.  
KW Mouse: T cell derived inducible factor; TIFalpha; ss; antiallergic;  
KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;  
KW cancer; lymphoma; immune system disorder; allergy; asthma;  
KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;  
KW thyroiditis; melanoma; hepatoma.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT CDS 52..591  
FT /\*tag= a  
FT /product= "TIFalpha"  
FT primer\_bind 106..126  
FT /\*tag= b  
FT /note= "PCR primer appearing as AAS14861"  
FT primer\_bind complement (764..784)  
FT /\*tag= c  
FT /note= "PCR primer appearing as AAS14862"  
PN US2001024652-A1.  
XX  
XX 27-SEP-2001.  
XX  
XX 29-DEC-2000; 2000US-0751797.  
XX 18-OCT-1999; 99US-0419568.  
XX 26-OCT-1998; 98US-0178973.  
PR

PR 16-JUL-1999; 99US-0354243.  
XX  
XX (DUMO/) DUMOUTIER L.  
PA (LOUA/) LOUAHED J.  
PA (RENA/) RENAULD J.  
XX  
XX Dumoutier L, Louahed J, Renauld J;  
XX  
XX WPI; 2001-638496/73.  
DR P-PSDB; AAU09090.  
XX  
XX New Isolated nucleic acid molecules encoding T cell inducible factors,  
XX useful as markers for expression or effect of interleukin (IL)-9 in a  
XX subject and diagnosing susceptibility to asthma or allergy  
XX  
XX Claim 1; Page 10; 26pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule, which encodes  
XX a T cell derived inducible factor (TIF) which are upregulated by the  
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor  
XX activation. The TIF proteins (or their mutants) may be used to test IL-9  
XX ant/agonists for their potency against lymphomas, immune system  
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),  
XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration  
XX or inhibit differentiation of tissue types in which they are active and  
XX therefore be used to develop treatments for melanomas and hepatomas.  
XX The present sequence encodes mouse TIFalpha.  
XX  
SQ Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;

Query Match 47.0%; Score 524.4; DB 22; Length 1119;  
Best Local Similarity 74.3%; Pred. No. 1.2e-104;  
Matches 819; Conservative 0; Mismatches 246; Indels 37; Gaps 11;  
Qy 15 tctgcaatggcgccctgcagaaatctgtgagctcttcttcttattgggacccctggccacc 74  
Db 46 tctctgagtgctgtcctgcagaaatctatgagtttctcttattgggacccctggccacc 105  
Qy 75 agctgcctctcttcttcttggccctcttggtagagggagagcagctgcgccatcagctcc 134  
Db 106 agctgcctctcttcttcttggccctcttggtagagggagagcagctgcgccatcagctcc 165  
Qy 135 cactgcagcttgacaagctccaaatctccagcagccttatataccaaacgcacccctctatg 194  
Db 166 cggtagcagcttgaggtgtccaaatctccagcagccttatataccaaacgcacccctctatg 225  
Qy 195 ctggctaaggagctgagcttggtgatacaacacacagacgtctctctcattggggagagaa 254  
Db 226 ctggccaaggagggcagccttgtagatacaacacacagacgtctcctcattggggagagaa 285  
Qy 255 ctgttccacggagtcagtagtgagcgtctctctgtagaagcaggtgctggaacttc 314  
Db 286 ctgttccagggagtcagtgctaaagatcagtgctcactgtagaagcaggtgctggaacttc 345  
Qy 315 acccttgaagaagtgctgttccctcaatctagtagttccagccttatatgcagaggttg 374  
Db 346 acccttgaagaagctgtctctccctcagtagagaggtttccagccttatatgcagaggttg 405  
Qy 375 gtgccttctctgcccagctcagcaacagctaaagcacatgtcatattgaaaggtgatgac 434  
Db 406 gtaccttctctgaccaaactcagcaatcagctcagctcctgtcacatcagcgttgacgac 465  
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Qy	795	tgtaacctgggttcatacacagaaaacaaatttattttttaataaatgtcttttccat	854
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Qy	915	taatacagacttttatattataaaatgtatttatattattataagaagctgaattttatta	974
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Db	977	tgcagtttataaatgagattttattatagaacaattatctgtattgata-tttagta	1035
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RESULT 15

AA009746	AA009746 standard; cdna; 778 BP.
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DE	Mouse zCYT018 cdna.
XX	
KW	Mouse; cytostatic; cytokine; zCYT018 protein; genetic abnormality;
KW	cancer; inflammation; gene therapy; ss.
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OS	Mus musculus.
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Key	Location/Qualifiers
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FT	sig_peptide
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XX	
XX	WO200146422-A1.
XX	
PN	28-JUN-2001.
XX	
PD	22-DEC-2000; 2000WO-US35308.
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PF	
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XX	23-DEC-1999; 99US-0471767.
PR	01-DEC-2000; 2000US-0250841.
XX	

[illegible]

Mon Sep 23 09:43:54 2002

Db 697 catcattagaagatttcacatgaaacctggctcagttgaaaaagaaa 744

Search completed: September 23, 2002, 00:43:53  
Job time: 4299 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:32:59 ; Search time 52.38 Seconds  
(without alignments)  
5233.429 Million cell updates/sec

Title: US-09-746-375-1  
Perfect score: 1116  
Sequence: 1 tcgagtagaattgtctgca.....ataaacacttgatccta ill16

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: Issued Patents NA.\*  
2: /cgn2\_6/ptodata/2/ina/5A-COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/5B-COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6A-COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/6B-COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/PCTUS-COMB.seq.\*  
7: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639	57.3	690	4	US-09-354-243B-24
2	525.2	47.1	1111	4	US-09-178-973B-9
3	525.2	47.1	1111	4	US-09-354-243B-9
4	524.4	47.0	1119	4	US-09-178-973B-7
5	524.4	47.0	1119	4	US-09-354-243B-7
6	216.4	19.4	5935	4	US-09-178-973B-17
7	216.4	19.4	5935	4	US-09-354-243B-29
8	215.6	19.3	7445	4	US-09-178-973B-8
9	215.6	19.3	7445	4	US-09-354-243B-8
10	207	18.5	4797	4	US-09-354-243B-25
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c 12	56.8	5.1	19124	2	US-08-487-826B-13
c 13	51.8	4.6	4254	2	US-08-443-639-7
c 14	51.8	4.6	8920	2	US-08-446-855A-1
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c 16	50.2	4.5	767	4	US-08-998-416-472
c 17	49	4.4	834	4	US-08-998-416-305
c 18	47.6	4.3	1368	3	US-08-874-563-5
c 19	47.6	4.3	1368	3	US-08-577-483-14
c 20	47.4	4.2	615	4	US-08-998-416-186
21	47.4	4.2	636	4	US-08-998-416-1137
c 22	47.4	4.2	701	4	US-08-998-416-701
23	47.4	4.2	837	4	US-08-998-416-288
24	46	4.1	782	4	US-09-007-119-15
c 25	45.6	4.1	615	4	US-08-998-416-186
c 26	45.6	4.1	636	4	US-08-998-416-1137
c 27	45.6	4.1	837	4	US-08-998-416-288

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30	45.6	4.1	1352	4	US-08-817-913-15	Sequence 15, Appl
31	45.6	4.1	1734	4	US-08-817-913-16	Sequence 16, Appl
32	45.6	4.1	1920	4	US-08-817-913-17	Sequence 17, Appl
33	45.4	4.1	1667	1	US-08-485-284A-1	Sequence 1, Appl
34	45	4.0	676	4	US-08-998-416-1014	Sequence 1014, Ap
35	45	4.0	677	4	US-08-998-416-920	Sequence 920, App
36	44.8	4.0	658	4	US-08-998-416-193	Sequence 193, App
c 37	44.6	4.0	665	2	US-08-883-795A-36	Sequence 36, Appl
c 38	44.6	4.0	26664	4	US-09-564-805-28	Sequence 28, Appl
c 39	44.6	4.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 40	44.6	4.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 41	44.6	4.0	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 42	44.2	4.0	828	4	US-08-998-416-538	Sequence 538, App
c 43	44.2	4.0	6124	4	US-08-213-419B-3	Sequence 3, Appli
c 44	44.2	4.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
45	44	3.9	3168	4	US-09-165-239A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-354-243B-24  
; Sequence 24, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louheid, Jamila  
; APPLICANT: Renaud, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible  
; TITLE OF INVENTION: (TIFS)  
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US09/178,973  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 24  
; LENGTH: 690  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-354-243B-24

Query Match 57.3%; Score 639; DB 4; Length 690;  
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Oy	61	ggaccctggccaccagctgcctctcttggccctctgtgacaggagagcagctg	120
Db	112	ggaccctggccaccagctgcctctcttggccctctgtgacaggagagcagctg	171
Oy	121	cgcccatcagctcccaactgcagcttgacaagtcacaaactccagcagcctatacca	180
Db	172	cgcccatcagctcccaactgcagcttgacaagtcacaaactccagcagcctatacca	231
Oy	181	accgacacttcagctggcttaaggaggtagcttggttgataaacacacagcgttcgc	240
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Oy	241	tcattggggagagaaactgttccacggagtcagtcagtcagtcagtcagtcagtcagtc	300
Db	292	tcattggggagagaaactgttccacggagtcagtcagtcagtcagtcagtcagtcagtc	351
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; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
US-09-354-243B-9

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Best Local Similarity 73.8%; Pred. No. 8.8e-12;
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QY 75 agctgctctctctcttctgtgagcgtctgtgtacaggaggagcgcgcgccatcagctcc 134
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QY 135 cactgagcgttgacaagctccaacttcagcagccctatatcaaccaacgcaccccttcag 194
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QY 315 acccttgaagaagtcgtctccctcaatctgatatggtttccacgcttatatgcaggaggtg 374
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QY 435 ctgcatatccagagaatgtgcagaagctgaaggacacagtcagtaaaagcttggaagaggt 494
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QY 495 ggagagataaagcaatggagaactggtgctgtttatgtctctgagaaatgccttcg 554
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QY 555 atttgaccagacgaagctgaaatgaataactaaaccccttccctgctgagaaataac 614
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QY 615 aattagatgcccaagcgaatttttttaacccaaaggagagtggaagcccaactccat 674
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Db 644 aataagatccctgaatggacttttta---ctaaaggaaagtgaagactaacgtccac 699

QY 675 catgatgggtgattccaaataaacccctgctgttagttacaaagaaacccaatgccaatt 734
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QY 735 ttgttttaaaagcagaagtgagctttcttaagcatagatatattattgataacatttcatt 794
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RESULT 4
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; Sequence 7, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; TITLE OF INVENTION: (TIPS)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543
; CURRENT APPLICATION NUMBER: US/09/178,973B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 7
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-178-973B-7

Query Match      47.0%; Score 524.4; DB 4; Length 1119;
Best Local Similarity 74.3%; Pred. No. 1.4e-121;
Matches 819; Conservative 0; Mismatches 246; Indels 37; Gaps 11;

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QY 75 agctgctctctctctgtgcccctctgtgtacaggaggagcagcgtcgcccatcagctcc 134
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QY 195 ctggctaaggagcgtagctgtgctgatacaacacagacagcttctcatttgaggagaaa 254
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QY 495 ggagagataaagcaatggagaactggtgctgtttatgtctctgagaaatgccttcg 554
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Db 586 gtctgagcagagaagactgagaaaacgaagaactgctccttctcgtcttctaaagaac 645
Qy 615 aattagatgcccacaaagcatttttttaaccacaaaggaagatgggaagccaaactccat 674
Db 646 aataagatccctgaatggactttttta----ctaaaggaaagtgaagtaaacgtccat 701
Qy 675 catgatgggtggtattccaaatgaaccctcggttagttacaaaggaacccaatgccactt 734
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Qy 735 ttgttttaagaccagagagtagactttctaaagcatagatgattattgataaacatttcat 794
Db 760 ttgtccatggagccag-aggtagacttgataaccacaaagattcatgacaatttttat 818
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Db 868 aaaggaggttacctctcatctcttta---gaaaaaaagcttatgaaacttca--tttcca 922
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Db 923 tatccaaattttattatgtaagttttattattattataagata-----cattttattta 976
Qy 975 tatcatttttaataatggattttattatagaacacatccatcagattgtcacttgagtg 1034
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RESULT
US-09-354-243B-7
; Sequence 7, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
; TITLE OF INVENTION: (TIPS)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 7
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
US-09-354-243B-7
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Query Match 47.0%; Score 524.4; DB 4; Length 1119;
Best Local Similarity 74.3%; Pred. No. 1.4e-121;
Matches 819; Conservative 0; Mismatches 246; Indels 37; Gaps 11;
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Qy 15 tctgcaatggccggccctgcagaaaatctgtgagctctttctcttatggggaccctgtgccacc 74
Db 46 tctctgggtgtccctgcagaaaatctatgattttcccttatggggactttgtggccgc 105
Qy 75 agctgcctctctcttggccctcttgggtacagggagagcagctggcccatcagctcc 134
Db 106 agctgcctgtctctctatgtccctgtggcccgagggcacaatgcgtgcgctccacaccc 165
Qy 135 cactgcaggcttgacaagtccaactccagcagccctatatcaccaaccgcaccttcattg 194
Db 166 cgggtgaagcttgaggtgtccaaactccagcagcgcgtacatcgtcaaccgcacatttatg 225
Qy 195 ctgctcaaggaggtagcttggctgataaacaacagacgcttctctcatggggagagaaa 254
Db 226 ctggccaaaggagcagccttgcagataaacaacagacgctccggtccatcggggagaaa 285
Qy 255 ctgttccacgagtcagatgagtgagcgtctctctctgtagaagcaggtgctgaacttc 314
Db 286 ctgttccgaggtgagtcagtgctaaagatcagtgctacctgtagaagcaggtgctcaactc 345
Qy 315 acccttgaagaagtgctgttccctccaatctgtgaggttccagccttatctatcagagggtg 374
Db 346 accctggaagagcttctgtctcccccagtcagacaggtttccagcctcatcagcaggggtg 405
Qy 375 gtgccccttctggccaggtcagcaacaggtcgaacacatgacacatgacatttgagggtgac 434
Db 406 gtaccttcttgacaaactcagcaatcagctcagctcgtctctcacatcagcgggagac 465
Qy 435 ctgcatactccagaggaatgtgcacaaagctgaagcacacagtgacaaagcttggagagagt 494
Db 466 cagaacatccagagaagatgtcagaaggtcgaaggagacagtgacaaagcttggagagagt 525
Qy 495 ggagagatcaaaagcaattgggagaactggtattgtgtttatgtctctctgagaaaatgcctgc 554
Db 526 ggagagatcaaggcgtatggggaaactggtgacactgctgtttatgtctctctgagaaatgcttgc 585
Qy 555 atttgaccagagcaaacgtgaaataatgataactaaaccccttccctctgctagaaaataac 614
Db 586 gtctgagcgaagaagctagaaaacgaagacgtcgtcttctctcgtctctgagaaatgcttgc 645
Qy 615 aattagatgcccacaaagcgtatttttttaacaaaggaagatgggaagccaaactccat 674
Db 646 aataagatccctgaatggactttttta----ctaaaggaaagtgaagactaacgtccat 701
Qy 675 catgatgggtggtattcccaaatgaacccctcggttagttacaaaggaacccaatgccactt 734
Db 702 catcattagaagatttcacatgaaacctggctcagttgaaaaagaaaatagtgctcaa--g 759
Qy 735 ttgtttataagaccagaggtagactttcttaagcagtagatatattattgataacatttcat 794
Db 760 ttgtccatgagaccag-aggttagacttgataacacaaagattcattgacaatatatttat 818
Qy 795 tgaactggtgtcttatcacacagaaaacaaatttttttaataaattgtctttttccat 854
Db 819 tgtcactgatg---atacaacagaaaaataatgacttttaaaaaattgtttt-----g 867
Qy 855 aaaaaagattacttccattcttcttggggaaaaaaccccttaaatagctttctgtttcca 914
Db 868 aaaggaggttacctctcatctcttta---gaaaaaaagcttatgtaacttca--tttcca 922
Qy 915 taatcagactttatttataaataatgattattattattataagacactgtttttat 974
Db 923 tatccaaattttattatgtaagttttattattattataagata-----cattttattta 976
Qy 975 tatcatttttaataatggattttattatagaacacatccatcagattgtcacttgagtg 1034
Db 977 tgtcagtttataatgattgtttattattatagaacacattctgtctattgata-tttagta 1035
Qy 1035 taaggctaattgtattattatgacaataatttatagagctataacatgtttattttgacct 1094
Db 1036 taaggcaata---atatattatgacaataactatgg-----aaacaagatatcttaggctt 1088
Qy 1095 caataaacacttggatatcccta 1116
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|||||  
Db 1089 taataaacatggatcatcata 1110

## RESULT

6

US-09-178-973B-17

: Sequence 17, Application US/09178973B

: Patent No. 6274710

: GENERAL INFORMATION:

: APPLICANT: Dumoutier, Laure

: APPLICANT: Louhed, Jamila

: APPLICANT: Renauld, Jean-Christophe

: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac

: TITLE OF INVENTION: (TIFs)

: FILE OF INVENTION: The Proteins Encoded, and Uses Thereof

: FILE REFERENCE: LUD 5543

: CURRENT APPLICATION NUMBER: US/09/178,973B

: PRIOR FILING DATE: 1998-10-26

: NUMBER OF SEQ ID NOS: 17

: SEQ ID NO 17

: LENGTH: 5935

: TYPE: DNA

: ORGANISM: Mus musculus

US-09-178-973B-17

Query Match 19.4%; Score 216.4; DB 4; Length 5935;

Best Local Similarity 69.9%; Pred. No. 1.3e-44;

Matches 446; Conservative 0; Mismatches 156; Indels 36; Gaps 10;

QY 479 aaagcttgagagagtgagagatcaaaagcaattggagaaactggattgtgtttatgtc 538

Db 5221 atagcttgagagagcgagagatcaaaagcgtcggaactggagactgtgtttatgtc 5280

QY 539 tctgagaaatgctgcatttgaccagagcaaaagctgaaataaataaccctctt 598

Db 5281 tctgagaaatgctgcatttgaccagagcaaaagctgaaataaataaccctctt 5340

QY 599 cctgtgagaataaacaattagatgcccaaaagcgatttttttaaccaaaaggaagtg 658

Db 5341 gcttctaaaaagaacaataaagatccctgaatggactttttt---actaaaggaagtg 5396

QY 659 ggaagccaactccatcatgatgggtggattcccaatgaaccctgcgttagttacaag 718

Db 5397 agaagtaacgtcccatcatttagaagatttcacatgaacacctggtcagttgaaag 5456

QY 719 gaaaccaatgccactttgtttataagaccagaaagtagaactttctaagcatattt 778

Db 5457 aaatagtgctcaa--gtgtccatgagaccag--aggtagacttgataccacaagattc 5513

QY 779 attgataacatttcattgtaactgggtgttctatcacagaaaaacaattttttaa 838

Db 5514 attgacaatttttattgtcattgat---aatgcaacagaaaaagtagtactttaaa 5569

QY 839 aattgtcttttccataaaaaagattacatttccattcctttgggggaaaaaacccctaa 898

Db 5570 aattgttt-----gaaagggaggttaccctctcctccta---gaagaaaagcctatg 5619

QY 899 tagcttcattgtcccaataacatcagtcatttatattataaagtattattattataa 958

Db 5620 taacttca--ttccataaccaataacttatatagtagttattattataagata- 5676

QY 959 gactgattttattatcatcatttataataggattttattattatagaacatcatcga 1018

Db 5677 -----cattttattattgtcagttattataataggattttattataagata 5731

QY 1019 tattgtacttgagtgaggtgtaattatgattattatgacaataattatagagctataa 1078

Db 5732 tgttgattttgagataaagcaata---atatattatgataataactatag---aaac 5784

QY 1079 catgtttatttgacctcaataaacaacttggatccta 1116

Db 5785 aagatatcttaggtgttttaataaacacatgaatcatcata 5822

## RESULT

7

US-09-354-243B-29

: Sequence 29, Application US/09354243B

: Patent No. 6359117

: GENERAL INFORMATION:

: APPLICANT: Dumoutier, Laure

: APPLICANT: Louhed, Jamila

: APPLICANT: Renauld, Jean-Christophe

: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible

: TITLE OF INVENTION: (TIFs)

: FILE OF INVENTION: The Proteins Encoded, and Uses Thereof

: FILE REFERENCE: LUD 5543.1

: CURRENT APPLICATION NUMBER: US/09/354,243B

: PRIOR FILING DATE: 1999-07-16

: PRIOR FILING DATE: 1998-10-26

: NUMBER OF SEQ ID NOS: 29

: SEQ ID NO 29

: LENGTH: 5935

: TYPE: DNA

: ORGANISM: Homo sapiens

: FEATURE:

US-09-354-243B-29

Query Match 19.4%; Score 216.4; DB 4; Length 5935;

Best Local Similarity 69.9%; Pred. No. 1.3e-44;

Matches 446; Conservative 0; Mismatches 156; Indels 36; Gaps 10;

QY 479 aaagcttgagagagtgagagatcaaaagcaattggagaaactggattgtgtttatgtc 538

Db 5221 atagcttgagagagcgagagatcaaaagcgtcggaactggagactgtgtttatgtc 5280

QY 539 tctgagaaatgctgcatttgaccagagcaaaagctgaaataaataaccctctt 598

Db 5281 tctgagaaatgctgcatttgaccagagcaaaagctgaaataaataaccctctt 5340

QY 599 cctgtgagaataaacaattagatgcccaaaagcgatttttttaaccaaaaggaagtg 658

Db 5341 gcttctaaaaagaacaataaagatccctgaatggactttttt---actaaaggaagtg 5396

QY 659 ggaagccaactccatcatgatgggtggattcccaatgaaccctgcgttagttacaag 718

Db 5397 agaagtaacgtcccatcatttagaagatttcacatgaacacctggtcagttgaaag 5456

QY 719 gaaaccaatgccactttgtttataagaccagaaagtagaactttctaagcatattt 778

Db 5457 aaatagtgctcaa--gtgtccatgagaccag--aggtagacttgataccacaagattc 5513

QY 779 attgataacatttcattgtaactgggtgttctatcacagaaaaacaattttttaa 838

Db 5514 attgacaatttttattgtcattgat---aatgcaacagaaaaagtagtactttaaa 5569

QY 839 aattgtcttttccataaaaaagattacatttccattcctttgggggaaaaaacccctaa 898

Db 5570 aattgttt-----gaaagggaggttaccctctcctccta---gaagaaaagcctatg 5619

QY 899 tagcttcattgtcccaataacatcagtcatttatattataaagtattattattataa 958

Db 5620 taacttca--ttccataaccaataacttatatagtagttattattataagata- 5676

QY 959 gactgattttattatcatcatttataataggattttattattatagaacatcatcga 1018

Db 5677 -----cattttattattgtcagttattataataggattttattataagata 5731

QY 1019 tattgtacttgagtgaggtgtaattatgattattatgacaataattatagagctataa 1078

Db 5732 tgttgattttgagataaagcaata---atatattatgataataactatag---aaac 5784

QY 1079 catgtttatttgacctcaataaacaacttggatccta 1116

Db 5785 aagatatcttaggtgttttaataaacacatgaatcatcata 1116

Mon Sep 23 09:43:55 2002

Db 5785 aagatatcttaggctttaataaacacatgaatatcata 5822

RESULT 8  
US-09-178-973B-8  
; Sequence 8, Application US/09178973B  
; Patent No. 6274710  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac  
; TITLE OF INVENTION: (Tifs)  
; FILE REFERENCE: LUD 5543  
; CURRENT APPLICATION NUMBER: US/09/178,973B  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 8  
; LENGTH: 7445  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-178-973B-8

Query Match 19.3%; Score 215.6; DB 4; Length 7445;  
Best Local Similarity 70.8%; Pred. No. 2.3e-44;  
Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;  
  
Qy 479 aaagcttgagagagtgagagatcaaaagcaattggagaaactggttgctgttatgctc 538  
Db 6535 atagcttgagagagtgagagatcaaaagcgattgggaaactggacctgctgttatgctc 6594  
  
Qy 539 tctgagaaatcctgcattgacagagcaagctgaaatgaataactaaactaaccccttt 598  
Db 6595 tctgagaaatcctgcattgacagagcaagctgaaatgaataactaaactaaccccttt 6654  
  
Qy 599 cctgctgagaaatacaactatgagtcgccccagagctgaaatgaataactaaactaaccccttt 658  
Db 6655 gccttctaaaaagaaataagatccctgaaatgagctgtttt---actaaaggaaagt 6710  
  
Qy 659 ggaagcacaactccatcatgattgggtgattcccaatgaacccctgcgttgattacaag 718  
Db 6711 agaagctaagctccatcatcattagaaagattccatgaacccctgcgttgattacaag 6770  
  
Qy 719 gaaaccaatgccaactttgtttataagaccagagtgagactttctaagcatagatat 778  
Db 6771 aaaaatagtgctcaa--gtgtccatgagaccag-aggtgagacttgataaccacaagattc 6827  
  
Qy 779 attgataacatttcattgtaactggtgtctctatcacagaaacaaatttttttaaat 838  
Db 6828 attgataacatttcattgtaactggtgtctctatcacagaaacaaatttttttaaat 883  
  
Qy 839 aattgtcttttccataaaaaagattactttccattcccttttaggggaaaaaacccctaaa 898  
Db 6884 aattgttt-----gaaaggaggttaacctctctcttta---gaaaaaagcttatg 6933  
  
Qy 899 tagctctcattgttccataatcagttactttattattataaattgtattattattataa 958  
Db 6934 taacttca--tttccatattccataattttattataatgtaagttattattataagata- 6990  
  
Qy 959 gactgcattttatttatcatcatttattataatgattattattattataagaacatcttca 1018  
Db 6991 -----cattttattatgctcagtttattataatgattattattattataagaacatcttca 7045  
  
Qy 1019 tattgctaacttgagtgtaaggcttaattattattattattattataagaacatcttca 1078  
Db 7046 tattgata-tttagtataaggcaata---atattattgacaataactatgg----aaac 7097  
  
Qy 1079 catgtttatttgacctcaataaacacttgatattccta 1116  
Db 7098 aagatatcttaggctttaataaacacatggatcata 7135

RESULT 9  
US-09-354-243B-8  
; Sequence 8, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; APPLICANT: Renauld, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible  
; TITLE OF INVENTION: (Tifs)  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354,243B  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US09/178,973  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 8  
; LENGTH: 7445  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
US-09-354-243B-8

Query Match 19.3%; Score 215.6; DB 4; Length 7445;  
Best Local Similarity 70.8%; Pred. No. 2.3e-44;  
Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;  
  
Qy 479 aaagcttgagagagtgagagatcaaaagcaattggagaaactggttgctgttatgctc 538  
Db 6535 atagcttgagagagtgagagatcaaaagcgattgggaaactggacctgctgttatgctc 6594  
  
Qy 539 tctgagaaatcctgcattgacagagcaagctgaaatgaataactaaactaaccccttt 598  
Db 6595 tctgagaaatcctgcattgacagagcaagctgaaatgaataactaaactaaccccttt 6654  
  
Qy 599 cctgctgagaaatacaactatgagtcgccccagagctgaaatgaataactaaactaaccccttt 658  
Db 6655 gccttctaaaaagaaataagatccctgaaatgagctgtttt---actaaaggaaagt 6710  
  
Qy 659 ggaagcacaactccatcatgattgggtgattcccaatgaacccctgcgttgattacaag 718  
Db 6711 agaagctaagctccatcatcattagaaagattccatgaacccctgcgttgattacaag 6770  
  
Qy 719 gaaaccaatgccaactttgtttataagaccagagtgagactttctaagcatagatat 778  
Db 6771 aaaaatagtgctcaa--gtgtccatgagaccag-aggtgagacttgataaccacaagattc 6827  
  
Qy 779 attgataacatttcattgtaactggtgtctctatcacagaaacaaatttttttaaat 838  
Db 6828 attgataacatttcattgtaactggtgtctctatcacagaaacaaatttttttaaat 883  
  
Qy 839 aattgtcttttccataaaaaagattactttccattcccttttaggggaaaaaacccctaaa 898  
Db 6884 aattgttt-----gaaaggaggttaacctctctcttta---gaaaaaagcttatg 6933  
  
Qy 899 tagctctcattgttccataatcagttactttattattataaattgtattattattataa 958  
Db 6934 taacttca--tttccatattccataattttattataatgtaagttattattataagata- 6990  
  
Qy 959 gactgcattttatttatcatcatttattataatgattattattattataagaacatcttca 1018  
Db 6991 -----cattttattatgctcagtttattataatgattattattattataagaacatcttca 7045  
  
Qy 1019 tattgctaacttgagtgtaaggcttaattattattattattattataagaacatcttca 1078  
Db 7046 tattgata-tttagtataaggcaata---atattattgacaataactatgg----aaac 7097  
  
Qy 1079 catgtttatttgacctcaataaacacttgatattccta 1116  
Db 7098 aagatatcttaggctttaataaacacatggatcata 7135

RESULT 10  
US-09-354-243B-25  
; Sequence 25, Application US/09354243B  
; Patent No. 6359117  
; GENERAL INFORMATION:  
; APPLICANT: Dumoutier, Laure  
; APPLICANT: Louhed, Jamila  
; APPLICANT: Renaud, Jean-Christophe  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors  
; TITLE OF INVENTION: (TIFS)  
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof  
; FILE REFERENCE: LUD 5543.1  
; CURRENT APPLICATION NUMBER: US/09/354.243B  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US09/178,973  
; PRIOR FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 25  
; LENGTH: 4797  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-354-243B-25

Query Match 18.5%; Score 207; DB 4; Length 4797;  
Best Local Similarity 100.0%; Pred. No. 2.7e-42;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 tggagttagaattgtctgcaatggcgcctgcagaaatctgtgagctcttccctatgg 60  
Db 52 tggagttagaattgtctgcaatggcgcctgcagaaatctgtgagctcttccctatgg 111  
Qy 61 ggaccctggcaccagctgcctctctctggccctctgtgacaggagagcagctg 120  
Db 112 ggaccctggcaccagctgcctctctctggccctctgtgacaggagagcagctg 171  
Qy 121 cgcccatcagctcccaactgcaggtgtgacaagtcacactccagcagccctatatcacc 180  
Db 172 cgcccatcagctcccaactgcaggtgtgacaagtcacactccagcagccctatatcacc 231  
Qy 181 accgcacctcagctgctgctaaggagg 207  
Db 232 accgcacctcagctgctgctaaggagg 258

RESULT 11  
US-09-056-075-1/c  
; Sequence 1, Application US/09056075  
; Patent No. 595368  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Eric A.  
; APPLICANT: Bradshaw, Marite  
; APPLICANT: Rood, Julian  
; TITLE OF INVENTION: Expression System for Clostridium  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,075

FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.95238  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6243 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 3770..4013  
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from  
OTHER INFORMATION: plasmid RP4"  
US-09-056-075-1

Query Match 5.7%; Score 63.2; DB 2; Length 6243;  
Best Local Similarity 48.9%; Pred. No. 1.9e-06;  
Matches 170; Conservative 0; Mismatches 178; Indels 0; Gaps 0;  
Qy 752 aggtagaattctcagaatagatatttattgatacaattctgttaactgggtcttat 811  
Db 1543 AAGTACCAATAAAACATTAGAACGTCATATTACGATATATGAAAAAATGGCTTTTAT 1484  
Qy 812 acacagaaacaattattttttaaataattgtctcttccataaaaaaagattacttcc 871  
Db 1483 AAGGCTCATTTTATATATCTTTCTCAAGATATATATATAATAAATAATTTTTC 1424  
Qy 872 attccttaggggaaacccctaaatagcttcttccataatcagctacttatat 931  
Db 1423 AAACCTTAAATAAAATAATTTTATATTTTATTTTATTTTATTTTATTTTATTTTAT 1364  
Qy 932 ttataaagtattattattattataagactgcatttatttattcatttatttataat 991  
Db 1363 TTTTATTTTATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1304  
Qy 992 ggattattattagaacatcattcgtattgtctactgtgagtgtaaggctaatatgata 1051  
Db 1303 ATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1244  
Qy 1052 ttatgacaataattatagagctataacatgtttatttgacctcaata 1099  
Db 1243 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1196

RESULT 12  
US-08-487-826B-13/c  
; Sequence 13, Application US/08487826B  
; Patent No. 5993827  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Kim L.  
; APPLICANT: Chitnis, Chetan  
; APPLICANT: Miller, Louis H.  
; APPLICANT: Peterson, David S.  
; APPLICANT: Su, Xin-zhaun  
; APPLICANT: Wellens, Thomas E.  
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe Martens Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: California  
; COUNTRY: US

ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israel, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH121.001CPI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-487-826B-13

Query Match 5.1%; Score 56.8; DB 2; Length 19124;  
Best Local Similarity 48.7%; Pred. No. 0.00011;  
Matches 154; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

Qy 779 attgataacatttcattgtaactggtgtctctacacagaaacattttttttaaatt 838  
Db 15773 ATTTTAAATTTTATTTTATGATATATATTTTATTTTAAATATATATTTTCTT 15714  
Qy 839 aattgtcttttccataaaaaagattcttccattcttaggggaaaaaacccctaaa 898  
Db 15713 TTTTGTGTTTATGATATATATTTTATTTTAAATGTTTTTTTCTCTCTTTT 15654  
Qy 899 tagcttcattgtccataacagacattttattataaaatgtatttattattataa 958  
Db 15653 GTTTTATTTTATTAATCAATTTTATTTTATATATAAAATTTTAAATTTTCTT 15594  
Qy 959 gactgcattttatttattatttattataatgattttattatagaacacattcga 1018  
Db 15593 GATAACTTTTCAATTTTATTTATCTCAAAATTTATATTTTATTAATTTTATT 15534  
Qy 1019 tattgtacttgagtgtaaggctaatattgatattttatgacaataattatagagctaaa 1078  
Db 15533 TTTTAAAAAATTTTCTCTTTTATTTTATTTTATTTTATTTTATTTTATTTT 15474  
Qy 1079 catgtttatttgacct 1094  
Db 15473 ATATTTCAATTTTCTT 15458

RESULT 13  
US-08-443-639-7/c  
Sequence 7, Application US/08443639  
Patent No. 5981843  
GENERAL INFORMATION:  
APPLICANT: Chappell, Joseph  
APPLICANT: Yin, Shaohui  
APPLICANT: Cornett, Catherine A.G.  
TITLE OF INVENTION: Transcriptional Control Sequences and  
METHODS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder

STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,639  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33878  
REFERENCE/DOCKET NUMBER: 69-94  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4254 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Nicotiana tabacum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1217..1327, 1455..1718, 1806..2182,  
LOCATION: 2259  
LOCATION: ..2477, 2609..2747, 2903..3148, 3262..3558)  
US-08-443-639-7

Query Match 4.6%; Score 51.8; DB 2; Length 4254;  
Best Local Similarity 49.0%; Pred. No. 0.0011;  
Matches 166; Conservative 0; Mismatches 172; Indels 1; Gaps 1;

Qy 690 ccaaatgaaccctgcttagttacaaaggaaacacattgcttcttataagacca 749  
Db 560 CAAAGTGTATGCTTTGTTTCTCCACACAAAAAATGAAATTTTAAATATATTAAT 501  
Qy 750 gaaggtagactttctaaagcatagattttattgataacatttcattgtaactggtctct 809  
Db 500 TCAAGTTAGTTTGTGAATTTAAATTTCTTTTGGTATCGCTCTAGTTTATATTTGTTT 441  
Qy 810 atcacagaaacattttattttaataattgctttttccataaaaaagattacttt 869  
Db 440 GATGACATAGGTATATATGATATCTTTTACGCCCTTTTATTTTCAAGAAAAAAGTTGCAT 381  
Qy 870 ccattccttaggggaaaaaacccctaaatagcttcattgtttccataaatcagctattat 929  
Db 380 GGTGCGCGCGCATGTACACACACACACACATACATTTATATATATATATATATATAT 321  
Qy 930 atttataaatgtattattattattattataagactgcattttatttatttatttattt 989  
Db 320 ATATATATATATATA-TATATATATATATATATATATATATATATATATATATAT 262  
Qy 990 atggatttattatagaacatcatctcgatattgctact 1028  
Db 261 CTTTTCACAAATTTTAGTGTATTTTCTGATTATATATAAT 223

RESULT 14  
US-08-446-855A-1  
Sequence 1, Application US/08446855A  
Patent No. 5849573  
GENERAL INFORMATION:  
APPLICANT: Stewart, Thomas S

APPLICANT: Flores, Maria V  
APPLICANT: O'Sullivan, William J  
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl  
TITLE OF INVENTION: phosphate synthetase II  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 1100 No. 5849573th Glebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,855A  
FILING DATE: 06-Jul-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 47-80  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4100  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8920 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic  
US-08-446-855A-1

Query Match 4.6%; Score 51.8; DB 2; Length 8920;  
Best Local Similarity 53.1%; Pred. No. 0.0015;  
Matches 110; Conservative 0; Mismatches 97; Indels 0; Gaps 0;  
QY 862 attactttccattccttttaggggaaaaaaccccccataagctgcttcattggtccataatcag 921  
DB 8452 ATTAACCTTCATCCATAACAACATCAAGTATAAATATATAAATAGTAATATAATA 8511  
QY 922 tactttattataaagtattattattattataaagactgcttcattggtccataatcatt 981  
DB 8512 TATAAT 8571  
QY 982 ttattaatggtatttattattatagaaacatcattgctacttgagtgtaaggct 1041  
DB 8572 ATATTAATAAATGTTTTTAAATATGATCATTAATATATATATATATATATATATAT 8631  
QY 1042 aatattgatattatgacaataattat 1068  
DB 8632 AATTTTGTATATATACAAATTTTAT 8658

RESULT 15  
US-09-150-741-1  
Sequence 1, Application US/09150741  
Patent No. 6183996  
GENERAL INFORMATION:  
APPLICANT: Stewart et al.  
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate  
Patent No. 6183996  
TITLE OF INVENTION: Synthetase II  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/150,741  
CURRENT FILING DATE: 1998-09-10  
EARLIER APPLICATION NUMBER: PL6380  
EARLIER FILING DATE: 1992-12-16

EARLIER APPLICATION NUMBER: AU93/00617  
EARLIER FILING DATE: 1993-12-02  
EARLIER APPLICATION NUMBER: 08/446,855  
EARLIER FILING DATE: 1995-07-06  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 8920  
TYPE: DNA  
ORGANISM: Plasmodium falciparum  
US-09-150-741-1

Query Match 4.6%; Score 51.8; DB 4; Length 8920;  
Best Local Similarity 53.1%; Pred. No. 0.0015;  
Matches 110; Conservative 0; Mismatches 97; Indels 0; Gaps 0;  
QY 862 attactttccattccttttaggggaaaaaaccccccataagctgcttcattggtccataatcag 921  
DB 8452 attactttccattccttcataacacatgaaaagtataaataataataataata 8511  
QY 922 tactttattataaagtattattattattataaagactgcttcattggtccataatcatt 981  
DB 8512 tataatataatataatataatataatataatataatataatataatataatata 8571  
QY 982 ttattaatggtatttattattatagaaacatcattgctacttgagtgtaaggct 1041  
DB 8572 atattaataaagtgttttttaataaataatgataatataatataatataatata 8631  
QY 1042 aatattgatattatgacaataattat 1068  
DB 8632 aattttgttatataacaaattttat 8658

Search completed: September 23, 2002, 00:45:14  
Job time: 4335 sec

\_\_\_\_\_

10/23/02



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:30:13 ; Search time 1735.48 Seconds  
(without alignments)  
8679.214 Million cell updates/sec

Title: US-09-746-375-1  
Perfect score: 1116  
Sequence: 1 tcgagtagaattgtctgca.....ataaacacttgatccta 1116

Scoring table: IDENTITY\_NUC  
Gapex 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpi:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vit:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257.8	23.1	700	11 AK005228	Mus muscu
2	90	8.1	256	9 AV030414	AV030414 AV030414
3	82.6	7.4	1101	12 CNS00EVL	AL069706 Drosophil
4	77.2	6.9	1101	12 CNS0039C	AL063921 Drosophil
5	74.6	6.7	1043	12 CNS0145P	AL103735 Drosophil
6	73.2	6.6	1001	12 CNS0155H	AL105023 Drosophil
7	73.2	6.6	1101	12 CNS00BO1	AL057419 Drosophil
8	71.2	6.4	1101	12 CNS00EVL	AL069706 Drosophil
9	71	6.4	944	12 BH163008	BH163008 ENTTF38TR
10	70.4	6.3	389	12 AQ104025	AQ104025 HS_3108_B
11	69.2	6.2	1092	12 CNS020K7	AL175696 Tetraodon
12	69	6.2	1225	12 CNS0161D	AL101671 Drosophil
13	68.6	6.1	1101	12 CNS00088	AL063632 Drosophil
14	68.2	6.1	639	12 CNS038CX	AL232458 Tetraodon
15	68.2	6.1	996	12 CNS00FUH	AL071063 Drosophil
16	67.8	6.1	963	9 AL566565	AL566565 AL566565
17	67.8	6.1	1092	12 CNS020K7	AL175696 Tetraodon

18	67.6	6.1	832	12 CNS011OK	AL100526 Drosophil
19	67.6	6.1	928	12 CNS00DKY	AL071865 Drosophil
20	67	6.0	843	12 CNS00CS1	AL059666 Drosophil
21	67	6.0	1101	12 CNS017KE	AL108152 Drosophil
22	66.2	5.9	842	12 CNS00ACO	AL055007 Drosophil
23	66.2	5.9	895	12 CNS06FSV	AL396821 T7 end of
24	65.8	5.9	928	12 CNS00DKY	AL071865 Drosophil
25	65.8	5.9	1101	12 CNS00FYG	AL071206 Drosophil
26	65.8	5.9	1101	12 CNS016LI	AL106896 Drosophil
27	65.6	5.9	895	12 CNS06FSV	AL396821 T7 end of
28	65.2	5.8	905	12 CNS00KHX	AL077798 Drosophil
29	65	5.8	307	12 CNS00A3W	AL054893 Drosophil
30	64.8	5.8	912	12 AZ551630	AZ551630 ENTMM37TF
31	64.8	5.8	1200	12 CNS016CO	AL106578 Drosophil
32	64.6	5.8	1167	12 CNS07360	AL427102 clone BA0
33	64.4	5.8	851	12 BH149587	BH149587 ENTQB44TR
34	64.4	5.8	524	12 CNS01U90	AL167541 Tetraodon
35	64.2	5.8	1190	12 CNS020N7	AL206908 Tetraodon
36	64	5.7	987	12 CNS014PQ	AL104456 Drosophil
37	64	5.7	1101	12 CNS00EO7	AL069440 Drosophil
38	64	5.7	1101	12 CNS00FYG	AL071206 Drosophil
39	63.8	5.7	1101	12 CNS00CYH	AL060100 Drosophil
40	63.6	5.7	845	12 AQ745537	AQ745537 HS_2272_A
41	63.6	5.7	1137	12 CNS071NS	AL423150 clone BA0
42	63.4	5.7	874	12 AZ669565	AZ669565 ENTMM69TF
43	63.2	5.7	687	12 BH133925	BH133925 ENTNS77TR
44	63.2	5.7	879	12 BH164743	BH164743 ENTNG84TF
45	63.2	5.7	897	12 BH151924	BH151924 ENTFF95TF

## ALIGNMENTS

### RESULT 1

AK005228	AK005228	700 bp	mRNA	linear	HTC 19-JAN-2002
LOCUS	Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04:interleukin 10-related T cell-derived inducible factor, full insert sequence.				
DEFINITION					
ACCESSION	AK005228	GI:12837639			
VERSION	AK005228.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (strain:C57BL/6J) adult male cerebellum cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2 (sites)				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3 (sites)				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Todawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				



Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-res@rtc.riken.go.jp  
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES  
 source  
 Location/Qualifiers  
 1..256  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="1500012D04"  
 /clone\_lib="Mus musculus adult C57BL/6J cerebellum"  
 /sex="male"  
 /tissue\_type="cerebellum"  
 /dev\_stage="adult"  
 BASE COUNT 88 a 29 c 41 g 98 t  
 ORIGIN

Query Match 8.1%; Score 90; DB 9; Length 256;  
 Best Local Similarity 72.1%; Pred. No. 3e-07;  
 Matches 147; Conservative 0; Mismatches 50; Indels 7; Gaps 2;  
 QY 910 tccataatcagctactttattataatgattattattattattattataagactgatttt 969  
 Db 60 TTTCCTTCCATAACCGATACCTTTATATATGAGTGTATTTATTATAAGTATACATTTT 119  
 QY 970 atttatcatctttattataatggattttatttagaacaacattcgtactt 1029  
 Db 120 ATTATGTCAGTTTATTAATATGATTTTATTATAGAAAATATCTGATGATATTT 179  
 QY 1030 gaggtaagcgaattattgattatttagacaataattatagactataacattttattt 1089  
 Db 180 GAGTATAAGCAAAATA--ATATTTATGATAATAACTATAG----AAACAAGATATCTTA 232  
 QY 1090 gacccaataaacacttgatc 1113  
 Db 233 GGCCTTAATAACACATGAATATC 256

RESULT 3  
 CNS00EVL  
 LOCUS  
 DEFINITION  
 Drosophila melanogaster 1101 bp DNA linear GSS 04-JUN-1999  
 BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 ACCESSION AL069706  
 VERSION AL069706  
 KEYWORDS GSS  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 1101)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))  
 COMMENT - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Hammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
 source  
 Location/Qualifiers  
 1..1101  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="RPCI-98"  
 /clone="BACR29B23"  
 /note="end : 77"  
 BASE COUNT 419 a 91 c 60 g 299 t 232 others  
 ORIGIN

Query Match 7.4%; Score 82.6; DB 12; Length 1101;  
 Best Local Similarity 35.7%; Pred. No. 7.7e-06;  
 Matches 139; Conservative 78; Mismatches 172; Indels 0; Gaps 0;  
 QY 713 acaaaaggaaacccatgcccactttgtttataagaccagaggttagactttctaagcatag 772  
 Db 698 AAAAAAAWATWAAWAAATWATAWATAAATTAATAAAWAAATAAAWAAWATAATAT 757  
 QY 773 atattttgataaacatttccattgtaactggttctctacacagacaaacattttttt 832  
 Db 758 WATATATATWTTTAAWAAWAAWTTATWATAWATAWAAWAAWATAAATAWATAWA 817  
 QY 833 ttaaataattgtctttttccataaaagattacttccattcctttaggggaaaaaac 892  
 Db 818 TWAAAWAAWATAWATAWATAWATAWAAWAAAAATWATAATWATAWATAWAAAA 877  
 QY 893 cctaaatagcttcagtttccataacagcactttattattataaagtattattatta 952  
 Db 878 AATAWTTTWTWTTTAAWAAWATAWATAWAAWAAAAWAAAAATAAAWAAW 937  
 QY 953 ttataagactgactttattattattattattattattattattattattattattatt 1012  
 Db 938 WTWATATTTTATTAATWTTATWATWATWATWATWATWATWATWATWATWATWAT 997  
 QY 1013 attcgatttgctacttgagtgtaagcgaattattattattattattattattattatt 1072  
 Db 998 AWTAWATATATTTATTAANWTTATTTTAAWAAWATAATATATWATAWTTWATAW 1057  
 QY 1073 ctataacatgtttatttgacctcaataa 1101  
 Db 1058 WAATTAATATATATATTAATAWATAWAAAA 1086

RESULT 4  
 CNS0039G  
 LOCUS  
 DEFINITION  
 Drosophila melanogaster 1101 bp DNA linear GSS 03-JUN-1999  
 BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 ACCESSION AL063921  
 VERSION AL063921  
 KEYWORDS GSS  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 1101)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))  
 COMMENT - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).



```

RESULT 6
LOCUS CNS0155H/c
DEFINITION CNS0155H 1001 bp DNA linear GSS 26-JUL-1999
BACFIN3C23 of DrosBAC library from Drosophila melanogaster (fruit
fly)), genomic survey sequence.
ACCESSION AL105023
VERSION AL105023.1 GI:5617037
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1001)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES             Location/Qualifiers
     source            1..1001
                        /organism="Drosophila melanogaster"
                        /plasmid="pBelOBAC11"
                        /db_xref="taxon:7227"
                        /clone_lib="DrosBAC"
                        /clone="BACFIN3C23"
                        /note="end : SP6"
     BASE COUNT        266 a   219 c   134 g   150 t   232 others
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KEYWORDS	GSS.
SOURCE	fruit fly. Drosophila melanogaster
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1101)
AUTHORS	Genoscope..
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with The Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamooser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers 1. 1101 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCI-98" /clone="BACR24D09" /note="end : T7"
FEATURES	
source	
BASE COUNT	420 a 56 c 48 g 261 t 316 others
ORIGIN	

[illegible]

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RESULT 9
BH163008/c
LOCUS
DEFINITION
    BH163008
    Entamoeba histolytica Sheared DNA linear GSS 24-sep-2001
    genomic, DNA sequence.
ACCESSION
    BH163008
    BH163008.1 GI:15736446
VERSION
    GSS.
KEYWORDS
    Entamoeba histolytica.
    Entamoeba histolytica
    Eukaryota; Entamoebidae; Entamoeba.
    1 (bases 1 to 944)
REFERENCE
    Loftus B., Wang, Z., Van Aken, S. and Fraser, C.
    Determination of clone end sequences from Entamoeba histolytica
    HMI:IMSS sheared DNA library (2001)
    Unpublished (2001)
    Contact: Brendan J Loftus
    Department of Eukaryotic Genomics
    The Institute for Genomic Research
    9712 Medical Center Dr., Rockville, MD 20850, USA
    Tel: 301 838 0208
    Fax: 301 838 3543
    Email: bjloftus@tigr.org
    Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
    DNA library
    Seq primer: M13-Reverse
    Class: Shotgun
    High quality sequence start: 13
    High quality sequence stop: 559.

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/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: pHOS1; Site:1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark, a
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barell, Oxford University Press, 1999)."
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BASE COUNT	430 a	67 c	197 g	250 t
ORIGIN				
Query Match	6.4%;	Score 71;	DB 12;	Length 944;
Best Local Similarity	50.4%;	Pred. NO. 0.0012;		
Matches 173;	Conservative	0;	Mismatches 170;	Indels 0; Gaps 0
QY 773	atatttattgataaacatttcattcggtgaacctggtctctacacagaaacaaattttttt	832		
Db 594	ATACCTTATTATTCCTATACCTTTATACCTTTATATGTTTATCTCTTCATCTCTTTATACC	535		
QY 833	ttaaataattgtctttttccataaaaaagatbacttccattcccttttaggggaaaaaac	892		
Db 534	TTAAATACTTCTATATATGTATATATATTTTATACCTTTATACCTTTATACCTTTTATATG	475		
QY 893	cctaaataagcttcagtttccataaacagtaacttatattataatgtattattattatta	952		
Db 474	TTTATATGTTTATATGTTTATATGTTTATATGTTTATATGTTTATATGTTTATATCTTTA	415		
QY 953	ttaataagactgcattttatttatcatatttttaataatggattttatttatgaagaacatc	1012		
Db 414	TATGTTTATATGTTTATATCTTTTATATCTTTTATATCTTTTATATCTTTTATATCT	955		
QY 1013	attcgatattgctacttgagtgtaaggcctaatttgatattttatgacaataattatagag	1072		

5-JUL-1999  
BAC

BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL106171  
VERSION AL106171.1 GI:5620504  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1225)  
AUTHORS Direct Submission  
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequence :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES  
source Location/Qualifiers  
1..1225  
/organism="Drosophila melanogaster"  
/plasmid="pBelOBAC11"  
/db\_xref="taxon:7227"  
/clone\_lib="DrosBAC"  
/clone="BACN15C18"  
/note="end : SP6"

BASE COUNT 266 a 128 c 38 g 368 t 425 others  
ORIGIN

Query Match 6.24; Score 69; DB 12; Length 1225;  
Best Local Similarity 31.64; Pred. No. 0.0029;  
Matches 135; Conservative 93; Mismatches 199; Indels 0; Gaps 0;

Qy 605 tagaaataacaattagatgcccaagcatttttttaaccacaaagaaagatgggaagc 664  
Db 774 KAAAMNAAHHWTTTYYWAAAYNNAATAATTTAAATCKCAAAAMAAWAAWMAAAAC 833  
Qy 665 caaacctcatcatgatgggtggtcccaatgaacccctgcgttagttacaaagaaacc 724  
Db 834 CCMCCVCKKKKKKKKKKKDDKDAKRARADRRKAAATAATAATAATAATAATAA 893  
Qy 725 aatgccacttttggtttaagacagaggttagactttcttaagcatagattttatgat 784  
Db 894 AAAAMWATTTTYYAYAWAAAYANATAAWWATTTTAAAWWAAWAAWAAWAAWTTTY 953  
Qy 795 aacatttcattgtaactgggtgtctcatcacagaaacacatttttttaataatgt 844  
Db 934 AAAAANAATWTAATAATTAATTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTT 1013  
Qy 845 ctttttccataaaagattacttccattcttccatttaggggaaacccctaaatagctt 904  
Db 1014 TTTTAAANAANAANAANAATAATTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTT 1073  
Qy 905 catgtttccataaactagctactttattataaaatgtattttattattataaagctgc 964  
Db 1074 ATTTAAWAAWATWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTT 1133  
Qy 965 attttattattatcatttttaataaattggattttattatagaacacattcogattgc 1024  
Db 1134 ATAAAAAATWTTTAAWAAATAATATATATATATATATATATATATATATATAT 1193  
Qy 1025 tacttga 1031  
Db 1194 WTWTWAA 1200

RESULT 13  
CNS000B8  
LOCUS  
DEFINITION BACR01A24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL063632  
VERSION AL063632.1 GI:4938680  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)  
AUTHORS Direct Submission  
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequence :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES  
source Location/Qualifiers  
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/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCI-98"  
/clone="BACR01A24"  
/note="end : TET3"

BASE COUNT 228 a 114 c 110 g 512 t 137 others  
ORIGIN

Query Match 6.1%; Score 68.6; DB 12; Length 1101;  
Best Local Similarity 39.8%; Pred. No. 0.0034;  
Matches 134; Conservative 47; Mismatches 156; Indels 0; Gaps 0;

Qy 755 tagactttctgaagcagatatttattgatacaatttcattgtaactgggtgtctatataca 814  
Db 734 TWTATWTTWTTWAAWATTTTWTWTTTATTTTAAATTTWATTTTAAATTTTAAATTT 793  
Qy 815 cagaaacacattattttttaaataattgctcttttccataaaaaaagattcttccatt 874  
Db 794 TTTTWTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 853  
Qy 875 ccttttaggggaaaaaacccctaaatagcttcattccataaactcagctactattatta 934  
Db 854 TTTATTAATAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 913  
Qy 935 taaatgtattattattattataaagactgcattttattattattattattattattattga 994  
Db 914 TWTWTTWTTWTTWAAWTTTATTTTWTWTTTATTTTATTTTATTTTATTTTATTTTAT 973  
Qy 995 tttattttatagaacacattcattcogattgctacttgagtgtaaggcctaataatgat 1054  
Db 974 TTTTAAATTTTATTTAAWATATTTATTTTAAWTTTATTTTATTTTATTTTATTTTAT 1033  
Qy 1055 atgacacataattatagactataacacattgtttattga 1091  
Db 1034 AWTWAAWATWATWTTTATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1070



RESULT	14
CNS038CX	
LOCUS	639 bp DNA linear GSS 15-MAY-2000
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 005C19 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	CNS038CX
VERSION	AL232458.1 GI:7891593
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetraodon nigroviridis.
ORGANISM	Tetraodon nigroviridis. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE	1 (bases 1 to 639)
AUTHORS	Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 639)
AUTHORS	Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 639)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .
FEATURES	Location/Qualifiers
source	1.. 639
	/organism="Tetraodon nigroviridis"
	/db_xref="taxon:99883"
	/clone_lib="005C19"
	/clone_lib="G"
	/note="Genoscope sequence ID : C0BG005A81OXD1-end : T7"
BASE COUNT	210 a 3 c 5 g 381 t 40 others
ORIGIN	
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Best Local Similarity	46.5%; Pred. No. 0.004;
Matches	Conservative 6; Mismatches 164; Indels 0; Gaps 0;
Qy 774	tattattgataacatttcattgttaactggcttctatcacagagaacaattattttt 833
Db	
43	TATTATTATTTTAAAACTTTAACTTATTATTATAAAAAAAAAATAAATAATTA 102
Qy 834	taaataattctttttccataaaaaagataactttccattccttaggggaaaacc 893
Db	
103	TAAATTTATTTTAAAAATAAAAATTAATTTNTAAWANTNNNANAATTTTTNTNN 162
Qy 894	ctaaatgacctcatgttccataatcgacttcttatatttaaagtattattatt 953
Db	
163	NNNNNAANNNAWAANAANAATTTTNATAAATWTNTANTAATTTATTTTAT 222
Qy 954	tataagactgaatttatttatcatcattttattaataatgattattattagaac 1013
Db	
223	TTTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 282
Qy 1014	tccgatattgctaacttgagtgtaaggccaatatgattattattatgcataat 1073
Db	
283	TTTTTATATTATATTTATTTATTTTATTTTATTTTATTTTATTTTATTT 342

Search completed: September 23, 2002, 00:02:37  
Job time: 1944 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 00:45:19 ; Search time 2215.22 Seconds  
(without alignments)  
10542.526 Million cell updates/sec

Title: US-09-746-375-1  
Perfect score: 1116  
Sequence: 1 tcgagttagaattgtctgca.....ataaacacttgatctccta 1116

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 14

Total number of hits satisfying chosen parameters: 151023

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_em.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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2	1116	100.0	1116	6	AX179578	Sequence
3	1114	99.8	1152	6	AX092422	Sequence
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ALIGNMENTS

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AUTHORS	1 (bases 1 to 1116)						
TITLE	Presnell, S.R., Xu, W., Kindsvogel, W. and Chen, Z.						
JOURNAL	Human cytokine receptor						
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DEFINITION AX179578
ACCESSION AX179578
VERSION AX179578.1 GI:15132010
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Presnell,S.R. and Kindsvogel,W.
TITLES Cytokine zcyto18
JOURNAL Patent: WO 0146422-A 1 28-JUN-2001;
ZymoGenetics, Inc. (US)
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ACCESSION AX092422  
VERSION AX092422.1 GI:13444525  
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SOURCE Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1152)  
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and

Wood,W.I.  
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JOURNAL Patent: WO 0116318-A 153 08-MAR-2001;  
Genentech, Inc. (US)  
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SOURCE Homo sapiens
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REFERENCE 1 (bases 1 to 1167)
AUTHORS Xie,M.H., Aggarwal,S., Ho,W.H., Foster,J., Zhang,Z., Stinson,J.,
Wood,W.I., Goddard,A.D. and Gurney,A.L.
TITLE Interleukin (IL)-22, a Novel Human Cytokine That Signals through
the Interferon Receptor-related Proteins CRF2-4 and IL-22R
J. Biol. Chem. 275 (40), 31335-31339 (2000)
JOURNAL 10875937
PUBMED 2 (bases 1 to 1167)
AUTHORS Xie,M.-H., Aggarwal,S., Ho,W.-H., Foster,J., Zhang,Z., Stinson,J.,
Wood,W.I., Goddard,A.D. and Gurney,A.L.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2000) Molecular Biology, Genentech Inc., 1 DNA
Way, South San Francisco, CA 94080, USA
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DEFINITION Sequence 44 from Patent WO0070049.
ACCESSION AX048204
VERSION AX048204.1 GI:11876994
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1132)
JOURNAL Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
Azimzai,Y., Lu,D.A. and Patterson,C.
EXTRACELLULAR signaling molecules
Patent: WO 0070049-A 44 23-NOV-2000;
Incyte Genomics, Inc. (US)
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location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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Best Local Similarity 99.7%; Pred. No. 0; Matches 1084; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
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LOCUS	Homo sapiens mRNA for Interleukin 22 (IL-22 gene).								
DEFINITION	AJ277247								
ACCESSION	AJ277247								
VERSION	IL-22 gene; Interleukin 22.								
KEYWORDS	human.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	1 (bases 1 to 690)								
AUTHORS	Dumoutier, L., Van Roost, E., Colau, D. and Renauld, J.C.								
TITLE	Human interleukin-10-related T cell-derived inducible factor: molecular cloning and functional characterization as an hepatocyte-stimulating factor								
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (18), 10144-10149 (2000)								
MEDLINE	20420346								
REFERENCE	2 (bases 1 to 690)								
AUTHORS	Renauld, J.C.								
TITLE	Direct Submission								
JOURNAL	Submitted (10-APR-2000) Renauld J.C., UCL 74 59, Ludwig Institute for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels, BELGIUM								

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ACCESSION AC022511  
VERSION AC022511.22 GI:14669924  
KEYWORDS HTG.  
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 133350)

AluBROOKS, S.L., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Benton, J., Blum, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowler, S., Brille, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dihn, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garza, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mel, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokwenkwu, S., Ogih, M., Okwono, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoostari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Zhou, J., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Zuchiatapati, R. and Gibbs, R.

Direct Submission

2 (bases 1 to 133350)

Worley, K.C.

Direct Submission

Submitted (03-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 133350)

Worley, K.C.

Direct Submission

Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 11, 2001 this sequence version replaced gi:12656660.

INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email [gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

#### ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smits and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

#### QUALSTAT-REPORT-----

----- Summary Statistics -----

Contig length: 150667

Phrap values in estimate: 149705

Average error rate (BCM-Phrap estimate): 1.52849e-05

Fraction of Phrap values less than 40: 0.0163388

Number of consensus changing edits: 83

Number of N's in consensus: 0

----- Consensus changing edits -----

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complement(23989..24349)
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repeat_region      complement(24350..24651)
/rpt_family="L2"
repeat_region      25393..25482

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Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 188243 AGCTTGGAGAGAGTGAGAGATCAAAAGCAATTGGAGAACTGGATTGCTGTATTGTCTC 188184

Oy 541 tgaagaatgcctgcatttgaccagagcaaaactgaaataaactaaaccccttcc 600
Db 188183 TCAGAAATGCCCTGCTATTGACGAGCAAGCTGAAATGAATTAACCTAACCCCTTTCC 188124

Oy 601 ctgctagaataaacaattagatgccccaagcgatttttttaacaaaaggaagatggg 660
Db 188123 CTGCTAGAAATAACAATTAGATGCCCAAGCGATTTTTTTTAAACCAAGGAAGATGGG 188064

Oy 661 aagccaaactccatcatgatgggtggatccaaatgaaccctcgcttagttacaaggga 720
Db 188063 AAGCCAAACTCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGA 188004

Oy 721 aaccaatccactttgttataagaccagagagtagacttcttaagcatagattattat 780
Db 188003 AACCAATGCCACTTTGTGTTTATAAGACCAGAGGAGTAGACTTTCTAAGCATAGATTATTAT 187944

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Db 187943 TGATAAATTTTCATGTAACCTGGTGTCTATACACAGAAAAACAATTTATTTTAAATAA 187884

Oy 841 ttgtcttttccataaaaaagatactcttccattcctttaggggaaaaaccccttaata 900
Db 187883 TTGTCTTTTCCATAAAAAGATTACTTCCATTCTTTAGGGGAAAAAACCCCTTAAATA 187824

Oy 901 gcttcattgttccataatcagcactttatttataaatgattattattattattataaga 960
Db 187823 GCTTCATGTTTCCATAATCAGTACTTTATTTATTAATGATTTATTATTATTATAAG 187764

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Oy 1021 ttgctacttgagtgtaaggctaatttgattttttatgacaataattatagactataaca 1080
Db 187703 TTGCTACTTGAGTGAAGGCTAATTGATATTATGACAAATTAATATAGACTATAACA 187644

Oy 1081 tgtttatttgacctcaataaacacttggtatcccta 1116
Db 187643 TGTTTATTGACCTCAATAAACACTTGGATATCCCTA 187608

RESULT 11
AC087562 LOCUS Pan troglodytes clone RP43-74117, WORKING DRAFT SEQUENCE, 31
DEFINITION Pan troglodytes clone RP43-74117, WORKING DRAFT SEQUENCE, 31
unordered pieces.
AC087562
VERSION AC087562.4 GI:14190648
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE chimpanzee.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 135146)
AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Albrooks, S.L., Anaratunge, H.C., Are, J.R., Banks, T., Barbara, J.,
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Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Unpublished
Direct Submission
2 (bases 1 to 135146)
Worley, K.C.
Submitted (10-JAN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza Houston, TX 77030, USA
On May 23, 2001 this sequence version replaced gi:12621390.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: ZUAE
Center clone name: RP43-74117
----- Summary Statistics
Sequencing vector: M13: L08821
Chemistry: Dye-terminator Big Dye: 51% of reads
Assemble program: Phrap: version 0.990329
Consensus quality: 134068 bases at least Q40
Consensus quality: 143074 bases at least Q30
Consensus quality: 148054 bases at least Q20
Estimated insert size: 144346; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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\* 103933 104033: gap of unknown length  
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VERSION IL-22 gene; Interleukin 22.  
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SOURCE human.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 5397)  
AUTHORS Dumoutier L., Van Roost E., Amey G., Michaux L. and Renaud J.C.  
IL-TIF/IL-22: genomic organization and mapping of the human and  
mouse genes  
JOURNAL Genes and immunity. 1 (8), 488-494 (2000)  
MEDLINE 21069354  
PUBMED 11197690  
REFERENCE 2 (bases 1 to 5397)  
AUTHORS Renaud J.C.  
TITLE Direct Submission  
JOURNAL Submitted (10-APR-2000) Renaud J.C., UCL 74.59, Ludwig Institute  
for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,  
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/notes="number 1b"
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/genes="IL-22"
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/genes="IL-22"
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BASE COUNT 1525 a 1007 c 1187 g 1678 t
ORIGIN

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Matches 207;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 1 tcgagttagaattgtctgcaatggccgacctgcagaaatctgtgagctcttccttatgg 60
Db 652 TCGAGTTAGAAATTGCTGCAATGGCCGCCCTGCAGAAATCTGTGAGCTCTTTCCCTTATGG 711
Qy 61 ggaccctggcacacagctgctctcttcttggccctctgtgtacaggagagcagctg 120
Db 712 GGACCTGGGCCACCAAGCTGCTCTCTCTTTGGGCCCTCTGTGTACAGGAGGAGCAGCTG 771
Qy 121 cgcacatcagctcccaactgcagctgtgcaagctgcaactccagcagcctatatcacca 180
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Db 832 ACCGCACCTTCATGCTGGCTAAGGAGG 858

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LOCUS Pan troglodytes clone RP43-74117, WORKING DRAFT SEQUENCE, 31
DEFINITION unordered pieces.
AC087562 AC087562
VERSION AC087562.4 GI:14190648
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## KEYWORDS

SOURCE  
ORGANISMREFERENCE  
AUTHORS

HTG; HTGS\_PHASE1; HTGS\_DRAFT.

Chimpanzee.

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

1 (bases 1 to 135146)

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Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,  
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Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 135146)

Worley,K.C.

Direct Submission

Submitted (10-JAN-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On May 23, 2001 this sequence version replaced gi:12621390.

----- Genome Center

Center: Baylor College Of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: ZUAE

Center clone name: RP43-74117

----- Summary Statistics

Sequencing vector: M13; L08821

Chemistry: Dye-terminator Big Dye; 49% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 134068 bases at least Q40

Consensus quality: 148054 bases at least Q20

Estimated insert size: 144346; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation



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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 31 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 10537: contig of 10537 bp in length  
\* 10538 10537: gap of unknown length  
\* 10638 16496: contig of 5859 bp in length  
\* 16497 16596: gap of unknown length  
\* 16597 22635: contig of 6039 bp in length  
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\* 22736 28745: contig of 6010 bp in length  
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\* 28846 34084: contig of 5239 bp in length  
\* 34085 34184: gap of unknown length  
\* 34185 39046: contig of 4862 bp in length  
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\* 75304 75404: gap of unknown length  
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\* 127913 128012: gap of unknown length  
\* 128013 130629: contig of 2617 bp in length  
\* 130630 130729: gap of unknown length  
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\* Location/Qualifiers

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VERSION AX179614.1 GI:15132040  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM  
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AUTHORS Presnell, S. R. and Kindsvogel, W.  
TITLE Cytokine zcytol8  
JOURNAL Patent: WO 0146422-A 37 28-JUN-2001;  
ZymoGenetics, Inc. (US)  
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SOURCE Unknown.  
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AUTHORS Dumoutier, L., Louhed, J. and Renaud, J.  
TITLE Antibodies which specifically bind T Cell inducible factors (TIFs)  
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